

# Sequence Listing

<110> Baker, Kevin P.  
 Botstein, David  
 Desnoyers, Luc  
 Eaton, Dan L.  
 Ferrara, Napoleone  
 Fong, Sherman  
 Gao, Wei-Qiang  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, Christopher J.  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Pan, James  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Smith, Victoria  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Watanabe, Colin K.  
 Williams, P. Mickey  
 Wood, William I.

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				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
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Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
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Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
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Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
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Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
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Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
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Pro	Lys	Ala	Val											

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 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro  
                   35                  40                  45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
                   50                  55                  60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
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 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
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                   95                  100                  105

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Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val		125	130	135
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Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro		155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly		170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro		185	190	195
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Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg		215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln		230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp		245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly		260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe		275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile		290	295	300
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Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn		350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser		365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr		380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe				

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Val	Glu	Lys	Val	Thr 425	Gln	His	Ile	His	Gly 430	Leu	Ser	Gly	Lys	Lys 435				
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Tyr	Glu	Tyr	Leu	Leu 470	Lys	Gln	Trp	Ile	Gln 475	Gly	Gly	Lys	Gln	Glu 480				
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Val	Glu	Ser	Leu	Phe 605	Tyr	Leu	Tyr	Arg	Val 610	Thr	Gly	Asp	Arg	Lys 615				
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Thr	Arg	Val	Pro	Ser 635	Gly	Gly	Tyr	Ser	Ser 640	Ile	Asn	Asn	Val	Gln 645				
Asp	Pro	Gln	Lys	Pro 650	Glu	Pro	Arg	Asp	Lys 655	Met	Glu	Ser	Phe	Phe 660				
Leu	Gly	Glu	Thr	Leu 665	Lys	Tyr	Leu	Phe	Leu 670	Leu	Phe	Ser	Asp	Asp 675				
Pro	Asn	Leu	Leu	Ser 680	Leu	Asp	Ala	Tyr	Val 685	Phe	Asn	Thr	Glu	Ala 690				

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<223> Synthetic construct.

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<210> 14  
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<212> DNA  
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<220>  
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<223> Synthetic construct.

<400> 14  
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<210> 15  
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Gly Pro Phe His	Val Ala Ser Pro Glu	Leu His Pro Leu Tyr	His		
	185	190	195		
Tyr Lys Thr Tyr	Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln	His		
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Arg Glu Asp Asp	Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly	Leu		
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Gln Leu Phe Arg	Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr	Phe		
	245	250	255		
Arg His Leu His	Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys	Arg		
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Gly Leu Asn Thr	Val Lys Tyr His Val	Ala Ser Arg Thr Ala	Leu		
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<210> 21  
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 <212> PRT  
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 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
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<210> 23

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<212> DNA

<213> Homo sapiens

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<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
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 <223> Transmembrane domain (type II).

<400> 24  
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 35 40 45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
 50 55 60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
 65 70 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
 80 85 90

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser		95	100	105
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile		110	115	120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp		125	130	135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg		140	145	150
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe		155	160	165
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg		170	175	180
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile		185	190	195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg		200	205	210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val		215	220	225
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu		230	235	240
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe		245	250	255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp		260	265	270
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu		275	280	285
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His		290	295	300
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln		305	310	315
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg		320	325	330
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser		335	340	345
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp		350	355	360
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln		365	370	375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro				

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Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
	590	595	600		
Ala Leu Lys Val	Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr		
	605	610	615		

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24







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<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser  
20 25 30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val  
35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg  
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys  
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp  
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala  
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly  
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu  
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser  
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu  
230 235 240

Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245						250					255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
			335											

<210> 34  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct

<400> 34  
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<210> 35  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 35  
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<210> 36  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 36



ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

ggcgagccct aactatccag gag 23

<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

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ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150

tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200

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caatctattc ttgccacatc aagggattgt tattccttta aaaaaaacc 300



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<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
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Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu  
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn  
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe  
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu  
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser  
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu  
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser  
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu  
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<211> 1594  
<212> DNA  
<213> Homo sapiens

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tgccaccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
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<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50		55		60
Ser Phe Ile Leu	Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr			
	65	70			75
Lys Tyr Phe Met	Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys			
	80	85			90
Phe Phe Asp Ser	Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu			
	95	100			105
Pro Asn Phe Leu	Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp			
	110	115			120
Asp Asn Ile Ala	Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp			
	125	130			135
Ser Asp Pro Ala	Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr			
	140	145			150
Ala Tyr Leu Asp	Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu			
	155	160			165
Asn Thr Ser Ile	Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe			
	170	175			180
Gly Lys Leu Ala	Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val			
	185	190			195
Arg Glu Asp Leu	Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn			
	200	205			210
Leu Gly Ile Phe	Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe			
	215	220			225
Arg Leu Arg Arg	Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala			
	230	235			240
Ile Asp Lys Cys	Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile			
	245	250			255
Val Glu Thr Lys	Ile Cys Gln Glu				
	260				

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

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<210> 45



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65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
230	235	240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn  
350 355 360  
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser  
365 370 375  
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly  
380 385 390  
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser  
395 400 405  
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
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<210> 53  
<211> 3580  
<212> DNA  
<213> Homo sapiens

<400> 53  
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<210> 54

<211> 280

<212> PRT

<213> Homo sapiens

<400> 54

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Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu	20	25	30	
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu	35	40	45	
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr	50	55	60	
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser	65	70	75	
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys	80	85	90	
Ile	Thr	Pro	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln	95	100	105		
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His	110	115	120	
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu	125	130	135	
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val	140	145	150	
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu	155	160	165	
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu	170	175	180	
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala	185	190	195	
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg	200	205	210	
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala	215	220	225	
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp	230	235	240	
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala	245	250	255	
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala	260	265	270	
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<210> 55  
<211> 2401  
<212> DNA  
<213> Homo sapiens

<400> 55  
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10006172.120601



Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr			290	295	

<210> 57  
 <211> 4277  
 <212> DNA  
 <213> Homo sapiens

<400> 57

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cagagtgcc aagcttacctg tgaggtgcgt gggaaccccc cgccctccgt 1400  
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gccctatctg attgtcgggg tegtctggg ctccatcggt ctcacatcg 2950  
 tcaccttcat ccccttctgc ttgtggaggg cctggtctaa gcaaaaacat 3000  
 acaacagacc tgggttttcc tcgaagtgcc cttccaccct cctgcccgt 3050  
 tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100  
 cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150  
 aataggggct gccctcggc tgcagtgggc taccggggca tgaagcccca 3200  
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 <211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
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Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
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His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
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Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
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Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
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Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val	Thr	Gly	Tyr	Asn 275	Lys	Thr	Arg	Phe	Leu 280	Leu	Ser	Asn	Leu	Leu 285
Ile	Asp	Thr	Thr	Ser 290	Glu	Glu	Asp	Ser	Gly 295	Thr	Tyr	Arg	Cys	Met 300
Ala	Asp	Asn	Gly	Val 305	Gly	Gln	Pro	Gly	Ala 310	Ala	Val	Ile	Leu	Tyr 315
Asn	Val	Gln	Val	Phe 320	Glu	Pro	Pro	Glu	Val 325	Thr	Met	Glu	Leu	Ser 330
Gln	Leu	Val	Ile	Pro 335	Trp	Gly	Gln	Ser	Ala 340	Lys	Leu	Thr	Cys	Glu 345
Val	Arg	Gly	Asn	Pro 350	Pro	Pro	Ser	Val	Leu 355	Trp	Leu	Arg	Asn	Ala 360
Val	Pro	Leu	Ile	Ser 365	Ser	Gln	Arg	Leu	Arg 370	Leu	Ser	Arg	Arg	Ala 375
Leu	Arg	Val	Leu	Ser 380	Met	Gly	Pro	Glu	Asp 385	Glu	Gly	Val	Tyr	Gln 390
Cys	Met	Ala	Glu	Asn 395	Glu	Val	Gly	Ser	Ala 400	His	Ala	Val	Val	Gln 405
Leu	Arg	Thr	Ser	Arg 410	Pro	Ser	Ile	Thr	Pro 415	Arg	Leu	Trp	Gln	Asp 420
Ala	Glu	Leu	Ala	Thr 425	Gly	Thr	Pro	Pro	Val 430	Ser	Pro	Ser	Lys	Leu 435
Gly	Asn	Pro	Glu	Gln 440	Met	Leu	Arg	Gly	Gln 445	Pro	Ala	Leu	Pro	Arg 450
Pro	Pro	Thr	Ser	Val 455	Gly	Pro	Ala	Ser	Pro 460	Lys	Cys	Pro	Gly	Glu 465
Lys	Gly	Gln	Gly	Ala 470	Pro	Ala	Glu	Ala	Pro 475	Ile	Ile	Leu	Ser	Ser 480
Pro	Arg	Thr	Ser	Lys 485	Thr	Asp	Ser	Tyr	Glu 490	Leu	Val	Trp	Arg	Pro 495
Arg	His	Glu	Gly	Ser 500	Gly	Arg	Ala	Pro	Ile 505	Leu	Tyr	Tyr	Val	Val 510
Lys	His	Arg	Lys	Gln 515	Val	Thr	Asn	Ser	Ser 520	Asp	Asp	Trp	Thr	Ile 525
Ser	Gly	Ile	Pro	Ala 530	Asn	Gln	His	Arg	Leu 535	Thr	Leu	Thr	Arg	Leu 540
Asp	Pro	Gly	Ser	Leu 545	Tyr	Glu	Val	Glu	Met 550	Ala	Ala	Tyr	Asn	Cys 555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg



560										565					570				
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln					
				575					580					585					
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Ser	Gln	Pro	Asp				
				590					595					600					
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile					
				605					610					615					
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg					
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Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys					
				635					640					645					
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile					
				650					655					660					
Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly					
				665					670					675					
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu					
				680					685					690					
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr					
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Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr					
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Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met					
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Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr					
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Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys					
				755					760					765					
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His					
				770					775					780					
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn					
				785					790					795					
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr					
				800					805					810					
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro					
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Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg					
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Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro					
				845					850					855					

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	935	940	945
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	950	955	960
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	965	970	975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	980	985	990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	1025	1030	1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	1040	1045	1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	1100	1105	1110
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 <213> Artificial

<220>  
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 <222> 1-25  
 <223> Synthetic construct.

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 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 60  
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<210> 61  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 61  
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<210> 62  
 <211> 1661  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 678  
 <223> unknown base

<400> 62  
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 cacgggccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150  
 tgctgctcct gctactgctg ctgctgctgc ggcagcccggt aaccgcgcgcg 200  
 gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250  
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<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63

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				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
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Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
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Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
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Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
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Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
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Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
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Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
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Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
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Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
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Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
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Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
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Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
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Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
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Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
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Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

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Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro												
				275					280					285												
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu												
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Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly												
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Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu												
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Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg												
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Ala	Val	Ile	Gly	Ser	Glu	Phe	Ile	Gly	Ile	Gly	Gly	Asn	Tyr	Asp												
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Gly	Thr	Gly	Arg	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr												
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Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Xaa	Trp	Ser	Glu	Glu												
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Gln	Val	Glu	Lys	Val	Arg	Glu	Glu	Ser	Arg	Ala	Gln	Ser	Pro	Val												
				410					415					420												
Glu	Ala	Glu	Phe	Pro	Tyr	Gly	Gln	Leu	Ser	Thr	Ser	Cys	His	Ser												
				425					430					435												
His	Leu	Val	Pro	Gln	Asn	Gly	His	Gln	Ala	Thr	His	Leu	Glu	Val												
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Thr	Lys	Gln	Pro	Thr	Asn	Arg	Val	Pro	Trp	Arg	Ser	Ser	Asn	Ala												
				455					460					465												
Ser	Pro	Tyr	Leu	Val	Pro	Gly	Leu	Val	Ala	Ala	Ala	Thr	Ile	Pro												
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<210> 64  
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 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

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<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150  
cgggtgtttg ctgggtgccc cagctgaagc caacaagagt tctgaagata 200  
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250  
tacaaccaga atgtatcca gaaggactgc aactgcctgc acgtggtgga 300  
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450  
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600





Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
65 70 75  
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
80 85 90  
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
95 100 105  
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
110 115 120  
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
125 130 135  
Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
140 145 150  
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
155 160 165  
Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
170 175 180  
Met Leu Ser

<210> 69  
<211> 3170  
<212> DNA  
<213> Homo sapiens

<400> 69  
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tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150  
tccctttgca ttcccacccc tccgggcttt gcgcttctct ggggaccccc 200  
tcgccgggag atggccgctg tgatgcggag caaggattcg tctgctgcc 250  
tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300  
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gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
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Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
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<211> 1809
<212> DNA
<213> Homo sapiens
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<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly	
				20					25					30	
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser	
				35					40					45	
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr	
				50					55					60	
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr	
				65					70					75	
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val	
				80					85					90	
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val	
				95					100					105	
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val	
				110					115					120	
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys	
				125					130					135	
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys	
				140					145					150	
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser	
				155					160					165	
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg	
				170					175					180	
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro	
				185					190					195	
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu	
				200					205					210	
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro	
				215					220					225	

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<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His  
80 85 90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His  
95 100 105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg  
110 115 120

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro  
125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu  
140 145 150

Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp  
155 160 165

Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu  
170 175 180

His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala  
185 190 195

Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser  
200 205 210

Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val  
215 220 225

Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln  
230 235 240

Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu  
245 250 255

Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu  
260 265 270

Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn  
275 280 285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg  
290 295 300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu  
305 310 315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp  
320 325 330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys  
335 340

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens





Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val
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				125					130					135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr
				140					145					150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe
				155					160					165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr
				170					175					180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met
				185					190					195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr
				200					205					210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp
				215					220					225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe
				230					235					240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu
				245					250					255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe
				260					265					270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser
				275					280					285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro
				290					295					300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val
				305					310					315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile
				320					325					330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe
				335					340					345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu
				350					355					360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn
				365					370					375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile
				380					385					390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys

				395					400					405	
Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser	
				410					415					420	
Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu	
				425					430					435	
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly	
				440					445					450	
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser	
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<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.
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<400> 80
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<210> 81
<211> 23
<212> DNA
<213> Homo sapiens
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<220>  
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<222> 1-23  
<223> Synthetic construct.
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<400> 81
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<210> 82
<211> 49
<212> DNA
<213> Artificial
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<220>  
<221> Artificial sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 82  
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$\langle 210 \rangle$	83
$\langle 211 \rangle$	1844







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Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
	545		550		555
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	560		565		

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr			

	320		325		330
His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val	335		340		345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr	350		355		360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val	365		370		375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg	380		385		390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro	395		400		405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn	410		415		420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val	425		430		435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp	440		445		450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu	455		460		465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser	470		475		480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val	485		490		495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe	500		505		510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu	515		520		525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr	530		535		540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn	545		550		555
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala	560		565		570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp	575		580		585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile	590		595		600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu	605		610		615









Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg	Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu			

	425		430		435
Asp Pro Ala Leu	Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly				
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Trp Val Leu Arg	Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys				
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Trp Pro Thr Pro	Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg				
	470		475		480
Met Pro Glu Gln	Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val				
	485		490		495
Ser Arg Ser Tyr	His Phe Gly Ile Val Gly Leu Asn Met Asn Gly				
	500		505		510
Tyr Phe His Glu	Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val				
	515		520		525
Pro Gly Val Gln	Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala				
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Tyr Glu Val Glu	Val His Arg Leu Leu Ser Glu Ala Glu Val Leu				
	545		550		555
Asp His Ser Lys	Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr				
	560		565		570
Glu Gly His Thr	Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp				
	575		580		585
Asp Phe Thr Thr	Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp				
	590		595		600
Asp Leu Asp Val	Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe				
	605		610		615
Arg Lys Lys Asn	His Phe Leu Val Val Gly Val Pro Ala Ser Pro				
	620		625		630
Tyr Ser Val Lys	Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu				
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Pro Pro Pro Lys	Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr				
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<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89



<400> 94

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<210> 95  
 <211> 307  
 <212> PRT  
 <213> Homo sapiens

<400> 95

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Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	
				35					40					45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	
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Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	
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Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	
				125					130					135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	
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Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	
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Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	
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Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	
				200					205					210	
Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	
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Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	

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<210> 96
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 96
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<210> 97
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 97
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<210> 98
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct.

<400> 98
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<210> 99
<211> 1429

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<212> DNA  
<213> Homo sapiens

<400> 99

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Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

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 <212> DNA  
 <213> Homo sapiens

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	170	175	180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	185	190	195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly				

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Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
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Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
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His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
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Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
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Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
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Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
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Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
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Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
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Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
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Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
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Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
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Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
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Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
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His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
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Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
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Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
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Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
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Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
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Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
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Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
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Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
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Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu	
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Ala	Ala	Ser	Gly	Leu	Ala	Leu	Leu	Leu	Trp	Lys	Pro	Val	Thr	Val	
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Leu	Val	Lys	Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu	
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Thr	Pro	Phe	Ser	Gly	Pro	Pro	Thr	Ser	Gln	Ala	Asp	Leu	Asp	Tyr	



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Val	Val	Pro	Gln	Ile 800	Tyr	Arg	His	Met	Gln 805	Glu	Glu	Phe	Arg	Gly 810
Arg	Leu	Glu	Arg	Thr 815	Lys	Ser	Gln	Gly	Pro 820	Leu	Thr	Val	Ala	Ala 825
Tyr	Gln	Leu	Gly	Ser 830	Val	Tyr	Ser	Ala	Ala 835	Met	Val	Thr	Ala	Leu 840
Thr	Leu	Leu	Ala	Phe 845	Pro	Leu	Leu	Leu	Leu 850	His	Ala	Glu	Arg	Ile 855
Ser	Leu	Val	Phe	Leu 860	Leu	Leu	Phe	Leu	Gln 865	Ser	Phe	Leu	Leu	Leu 870
His	Leu	Leu	Ala	Ala 875	Gly	Ile	Pro	Val	Thr 880	Thr	Pro	Gly	Pro	Phe 885
Thr	Val	Pro	Trp	Gln 890	Ala	Val	Ser	Ala	Trp 895	Ala	Leu	Met	Ala	Thr 900
Gln	Thr	Phe	Tyr	Ser 905	Thr	Gly	His	Gln	Pro 910	Val	Phe	Pro	Ala	Ile 915
His	Trp	His	Ala	Ala 920	Phe	Val	Gly	Phe	Pro 925	Glu	Gly	His	Gly	Ser 930
Cys	Thr	Trp	Leu	Pro 935	Ala	Leu	Leu	Val	Gly 940	Ala	Asn	Thr	Phe	Ala 945
Ser	His	Leu	Leu	Phe 950	Ala	Val	Gly	Cys	Pro 955	Leu	Leu	Leu	Leu	Trp 960
Pro	Phe	Leu	Cys	Glu 965	Ser	Gln	Gly	Leu	Arg 970	Lys	Arg	Gln	Gln	Pro 975
Pro	Gly	Asn	Glu	Ala 980	Asp	Ala	Arg	Val	Arg 985	Pro	Glu	Glu	Glu	Glu 990
Glu	Pro	Leu	Met	Glu 995	Met	Arg	Leu	Arg	Asp 1000	Ala	Pro	Gln	His	Phe 1005
Tyr	Ala	Ala	Leu	Leu 1010	Gln	Leu	Gly	Leu	Lys 1015	Tyr	Leu	Phe	Ile	Leu 1020
Gly	Ile	Gln	Ile	Leu 1025	Ala	Cys	Ala	Leu	Ala 1030	Ala	Ser	Ile	Leu	Arg 1035
Arg	His	Leu	Met	Val 1040	Trp	Lys	Val	Phe	Ala 1045	Pro	Lys	Phe	Ile	Phe 1050
Glu	Ala	Val	Gly	Phe 1055	Ile	Val	Ser	Ser	Val 1060	Gly	Leu	Leu	Leu	Gly 1065
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<212> DNA  
<213> Homo sapiens

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<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
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Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
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Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
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Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
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Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
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Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
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Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
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Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
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Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
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Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
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Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
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Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
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<212> PRT

<213> Homo sapiens

<400> 111

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Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
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Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
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Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
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Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
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Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
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Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
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Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
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<400> 113  
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 <212> PRT  
 <213> Homo sapiens

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 50 55 60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
 65 70 75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
 80 85 90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
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 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
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 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
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 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
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 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
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 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
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 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
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 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
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Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
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Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
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530

535

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&lt;210&gt; 119

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-23

&lt;223&gt; Synthetic construct.

&lt;400&gt; 119

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&lt;210&gt; 120

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-24

&lt;223&gt; Synthetic construct.

&lt;400&gt; 120

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&lt;210&gt; 121

&lt;211&gt; 49

&lt;212&gt; DNA

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&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-49

&lt;223&gt; Synthetic construct.

&lt;400&gt; 121

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&lt;210&gt; 122

&lt;211&gt; 1778

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

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 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60  
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 65 70 75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
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 125 130 135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165  
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 170 175 180  
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
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 200 205 210  
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
 215 220 225  
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100017212001

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcattctatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens





Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480
Pro	Val	Ser	Gln														

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens



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 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600  
 ctctcctcc ttgcatatct cctactgccc tccagcctga gtgatagagt 1650  
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700  
 gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750  
 tccatctcct tagttttctt ttaaggtgac ccatctgtga taaaaatata 1800  
 gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850  
 aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900  
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950  
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagtctga 2000  
 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050  
 attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100  
 tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150  
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 aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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Val	Ala	Leu	Leu	Ile	Val	Cys	Asp	Val	Pro	Ser	Ala	Ser	Ala	Gln
				20					25					30

Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35					40					45

Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
				50					55					60

Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
				65					70					75

Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
				80					85					90

Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
				95					100					105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
				320					325					330	
Ser	Phe	Leu	Met	Ser											
				335											

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 ctgctaggga gagaacgcca gagggaggcg gctggcccg cggcaggctc 100







Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

	365		370		375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe	Lys		
	380	385	390		
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu	Ser		
	395	400	405		
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu	Arg		
	410	415	420		
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser	Ile		
	425	430	435		
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu	Thr		
	440	445	450		
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp	Gln		
	455	460	465		
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser	Val		
	470	475	480		
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser	Ile		
	485	490	495		
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His	Gln		
	500	505	510		
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp	Gln		
	515	520	525		
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val			
	530	535			

<210> 133

<211> 1475

<212> DNA

<213> Homo sapiens

<400> 133

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gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150

ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200

tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250

gttggtcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300

catcaccag tgtgacatct atagaccct tctgggcctg cccgctgaca 350

tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400

gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450



50										55					60				
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala					
				65					70					75					
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile					
				80					85					90					
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr					
				95					100					105					
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala					
				110					115					120					
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro					
				125					130					135					
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro					
				140					145					150					
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr					
				155					160					165					
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile					
				170					175					180					
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr					
				185					190					195					
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg					
				200					205					210					
Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser					
				215					220					225					
Leu	Thr	Gly	Tyr	Val															
				230															

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<210> 135
<211> 610
<212> DNA
<213> Homo sapiens
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<400> 135
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aagtcatcgc tcccgcgtggc tcagaaccat ggctgtgcca gccggcacc 150
agggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
cgccatcgtg tcctgagcgc agaccgcga atgtggtccc cctgcacct 250
tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300
gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350
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atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
 65 70 75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
 80 85 90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
 95 100 105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
 110 115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtctgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgcga ctcagcccgg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
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 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
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<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
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 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met  
 20 25 30  
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp  
 35 40 45  
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val  
 50 55 60  
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg  
 65 70 75  
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu  
 80 85 90  
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu  
 95 100 105  
 Cys Arg Ser Val Ser  
 110

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139



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 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
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 cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300  
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 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400  
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 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050  
 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150  
 gtggcctcct tggcctcggc cctgggttccc tccctcctgc tctgggctca 1200  
 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
 atggggatgc tggacggctc agcccctgtt ccaaggattt tggggtgctg 1300  
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450







Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	
				20					25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	
				35					40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	
				50					55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	
				65					70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	
				80					85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	
				95					100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	
				110					115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450
Thr		

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
 ctacgctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50  
 cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100  
 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gtcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400  
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500  
 gtgagctgcc gtogggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 ttttaaggctcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
 35 40 45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
 50 55 60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
 65 70 75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
 80 85 90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50  
 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100  
 caggctgcca tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtcttg agcgggaggt agactatctg 400





aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp  
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met  
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln  
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn  
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala  
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu  
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro  
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys  
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys  
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg  
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln  
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala  
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala  
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr  
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro  
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln  
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser  
245 250 255

1000617e.100601

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50  
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100  
 gttctcctct tctctotaat ccatccgtca cctctcctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttgggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
 gtttctctgc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg	gcctctatgg	gtgcaggatt	agttcccagt	cttactacca	550
gaaggccatc	tgggagctac	aggtgtcagc	actgggctca	gttcctctca	600
tttccatcac	gggatatgtt	gatagagaca	tccagctact	ctgtcagtcc	650
tcgggctggt	tccccgggcc	cacagcgaag	tggaaaggtc	cacaaggaca	700
ggatttgtcc	acagactcca	ggacaaacag	agacatgcat	ggcctgtttg	750
atgtggagat	ctctctgacc	gtccaagaga	acgccgggag	catatcctgt	800
tccatgcggc	atgctcatct	gagccgagag	gtggaatcca	gggtacagat	850
aggagatacc	tttttcgagc	ctatatcgtg	gcacctggct	accaaagtac	900
tgggaataact	ctgctgtggc	ctatTTTTTt	gcattgttgg	actgaagatt	950
ttcttctcca	aattccagt	gaaaatccag	gcggaactgg	actggagaag	1000
aaagcacgga	caggcagaat	tgagagacgc	ccggaaacac	gcagtggagg	1050
tgactctgga	tccagagacg	gctcacccga	agctctgcgt	ttctgatctg	1100
aaaactgtaa	cccatagaaa	agctccccag	gaggTgcctc	actctgagaa	1150
gagatttaca	aggaagagtg	tggTggcttc	tcagagtttc	caagcagggg	1200
aacattactg	ggaggTggac	ggaggacaca	ataaaaggTg	gcgcgtggga	1250
gtgtgccggg	atgatgtgga	caggaggaag	gagtacgtga	ctttgtctcc	1300
cgatcatggg	tactgggtcc	tcagactgaa	tggagaacat	ttgtatttca	1350
cattaaatcc	ccgtttttatc	agcgtcttcc	ccaggacccc	acctacaaaa	1400
ataggggtct	tcttggaacta	tgagtgtggg	accatctcct	tcttcaacat	1450
aatgaccag	tccottattt	ataccctgac	atgtcggttt	gaaggcttat	1500
tgaggcccta	cattgagtat	ccgtcctata	atgagcaaaa	tggaaactccc	1550
atagtcatct	gcccagtcac	ccaggaatca	gagaaaagg	cctcttggca	1600
aagggcctct	gcaatcccag	agacaagcaa	cagtgagtcc	tcttcacagg	1650
caaccacgcc	cttctctccc	aggggtgaaa	tgtaggatga	atcacatccc	1700
acattcttct	ttagggatat	taaggTctct	ctcccagatc	caaagtcccg	1750
cagcagccgg	ccaaggTggc	ttccagatga	agggggactg	gcctgtccac	1800
atgggagtca	ggtgtcatgg	ctgccctgag	ctgggaggga	agaaggctga	1850
cattacattt	agtttTctct	cactccatct	ggctaagtga	tcttgaaata	1900
ccacctctca	ggtgaagaac	cgtcaggaat	tcccatctca	caggctgtgg	1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
acagagtgtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050  
aa 2052

<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148  
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly  
1 5 10 15  
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala  
20 25 30  
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
35 40 45  
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
50 55 60  
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
65 70 75  
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
80 85 90  
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
95 100 105  
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
110 115 120  
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
125 130 135  
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
140 145 150  
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
155 160 165  
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
170 175 180  
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
185 190 195  
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
200 205 210  
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
215 220 225  
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

	230		235		240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys			
	245	250			255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp			
	260	265			270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys			
	275	280			285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys			
	290	295			300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro			
	305	310			315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val			
	320	325			330
Val Ala Ser Gln	Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val			
	335	340			345
Asp Gly Gly His	Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp			
	350	355			360
Asp Val Asp Arg	Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His			
	365	370			375
Gly Tyr Trp Val	Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr			
	380	385			390
Leu Asn Pro Arg	Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr			
	395	400			405
Lys Ile Gly Val	Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe			
	410	415			420
Phe Asn Ile Asn	Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg			
	425	430			435
Phe Glu Gly Leu	Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn			
	440	445			450
Glu Gln Asn Gly	Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu			
	455	460			465
Ser Glu Lys Glu	Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu			
	470	475			480
Thr Ser Asn Ser	Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu			
	485	490			495
Pro Arg Gly Glu	Met				
	500				

<210> 149

<211> 24

<212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 149  
 gcgtggtcca cctctacagg gacg 24

<210> 150  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 150  
 ggaactgacc cagtgtgac acc 23

<210> 151  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 151  
 gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
 <211> 2294  
 <212> DNA  
 <213> Homo sapiens

<400> 152  
 gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggcttcctt 50  
 ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
 aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
 gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
 gcctcggcgg ggaatgtcac cgttgccggc ggggcgcgcg ggcaggtgga 250  
 cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
 gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350  
 accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctcttt	tgggcgactg	ctggaccctc	ttccaccacc	tttcaggcgc	450
cgctcggccc	ctcgccgacc	acccctccgg	cggcggaaacg	cacttcgacc	500
acctctcagg	cgccgaccag	acccgcgcgg	accacccttt	cgacgaccac	550
tggcccggcg	cogaccaccc	ctgtagcgac	caccgtaccg	gcgcccacga	600
ctccccggac	cccgaccccc	gatctcccca	gcagcagcaa	cagcagcgtc	650
ctccccaccc	cacctgccac	cgaggccccc	tcttcgcctc	ctccagagta	700
tgtatgtaac	tgtctctgtg	ttggaagcct	gaatgtgaat	cgctgcaacc	750
agaccacagg	gcagtgtgag	tgtcggccag	gttatcaggg	gcttcactgt	800
gaaacctgca	aagaggggctt	ttacctaaat	tacactttctg	ggctctgtca	850
gccatgtgac	tgtagtccac	atggagctct	cagcataccg	tgcaacaggt	900
aagcaacaga	gggtggaact	gaagttttatt	ttatttttagc	aagggaaaaa	950
aaaaggctgc	tactctcaag	gaccatactg	gtttaaacaa	aggaggatga	1000
gggtcataga	tttacaaaat	attttatata	cttttattct	cttactttat	1050
atgttatatt	taatgtcagg	atttaaaaac	atctaattta	ctgatttagt	1100
tcttcaaaag	cactagagtc	gccaattttt	ctctgggata	atttctgtaa	1150
atttcatggg	aaaaaattat	tgaagaataa	atctgctttc	tggaagggct	1200
ttcaggcatg	aaacctgcta	ggaggttttag	aaatgttctt	atgtttatta	1250
atataccatt	ggagtttgag	gaaatttggt	gtttggttta	tttttctctc	1300
taatcaaaat	tctacatttg	tttctttgga	catctaaagc	ttaacctggg	1350
ggtaccctaa	tttatttaac	tagtggttaag	tagactgggt	ttactctatt	1400
taccagtaca	tttttgagac	caaaagtaga	ttaagcagga	attatcttta	1450
aactattatg	ttatttgagg	gtaatttaat	ctagtggaat	aatgtactgt	1500
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tatgtgaggc	acttggcctt	ttgtggaccc	caagtcaaaa	aactgaagag	1600
acagtattaa	ataatgaaaa	aaataatgac	aggttatact	cagtgttaacc	1650
tgggtataac	ccaagatctg	ctgccactta	cgagctgtgt	tccttgggca	1700
agtaatttcc	tttcaactgag	cttgtttctt	ctcaaggttg	ttgtgaagat	1750
taaatgagtt	gatatatata	aatgcctag	cacatgtcac	tcaataaatt	1800
ctggtttggt	ttaatttcaa	aqgaatatta	tggactgaaa	tgagagaaca	1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atactttagc 1900  
 actaaatatt ttaaagtgtt tataaatgat attatactgt tatggaatat 1950  
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
 ctcacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050  
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctc 2100  
 ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150  
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200  
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 agagggagac tctgtottaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro



	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255

Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 154  
 aactgctctg tggttggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgagcag ttagacacgtg ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggcctt ggtctcgggtg cccagggccc aggcctgtgtg gttgggaaga 100  
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150  
 ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200  
 tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcctgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgccca tcattctcac tcagctggag 400  
 ttcgggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttctctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600  
 gggctctgtg acctcggcca gtgtccaccc acctcgtca gcggtccc 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
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 gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa 100  
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150  
 gtccatgtgc cctgctcctt ctccataccc tcgcatggct ggatttacc 200  
 tggcccagta gttcatggct actggttccg ggaaggggccc aatacagacc 250  
 aggatgctcc agtyggccaca aacaaccag ctcgggcagt gtgggaggag 300  
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
 cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400  
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
 gtgagcagg gacacccct atgatctcct ggataggac ctccgtgtcc 600  
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650  
 gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
 tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900  
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
 gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100  
 tggagccaca gccctgggtc tcctgtcctt ctgcgtcatc ttcgttgtag 1150  
 tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcagggggc 1250  
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300  
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttcacaga tggatgaagcc ttgggactcg cggggacagg aggccactga 1400  
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550  
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
 tcaaactga atccacactg tgcctccct tttatTTTTT taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
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Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

				110					115					120
Met	Glu	Lys	Gly	Ser 125	Ile	Lys	Trp	Asn	Tyr 130	Lys	His	His	Arg	Leu 135
Ser	Val	Asn	Val	Thr 140	Ala	Leu	Thr	His	Arg 145	Pro	Asn	Ile	Leu	Ile 150
Pro	Gly	Thr	Leu	Glu 155	Ser	Gly	Cys	Pro	Gln 160	Asn	Leu	Thr	Cys	Ser 165
Val	Pro	Trp	Ala	Cys 170	Glu	Gln	Gly	Thr	Pro 175	Pro	Met	Ile	Ser	Trp 180
Ile	Gly	Thr	Ser	Val 185	Ser	Pro	Leu	Asp	Pro 190	Ser	Thr	Thr	Arg	Ser 195
Ser	Val	Leu	Thr	Leu 200	Ile	Pro	Gln	Pro	Gln 205	Asp	His	Gly	Thr	Ser 210
Leu	Thr	Cys	Gln	Val 215	Thr	Phe	Pro	Gly	Ala 220	Ser	Val	Thr	Thr	Asn 225
Lys	Thr	Val	His	Leu 230	Asn	Val	Ser	Tyr	Pro 235	Pro	Gln	Asn	Leu	Thr 240
Met	Thr	Val	Phe	Gln 245	Gly	Asp	Gly	Thr	Val 250	Ser	Thr	Val	Leu	Gly 255
Asn	Gly	Ser	Ser	Leu 260	Ser	Leu	Pro	Glu	Gly 265	Gln	Ser	Leu	Arg	Leu 270
Val	Cys	Ala	Val	Asp 275	Ala	Val	Asp	Ser	Asn 280	Pro	Pro	Ala	Arg	Leu 285
Ser	Leu	Ser	Trp	Arg 290	Gly	Leu	Thr	Leu	Cys 295	Pro	Ser	Gln	Pro	Ser 300
Asn	Pro	Gly	Val	Leu 305	Glu	Leu	Pro	Trp	Val 310	His	Leu	Arg	Asp	Ala 315
Ala	Glu	Phe	Thr	Cys 320	Arg	Ala	Gln	Asn	Pro 325	Leu	Gly	Ser	Gln	Gln 330
Val	Tyr	Leu	Asn	Val 335	Ser	Leu	Gln	Ser	Lys 340	Ala	Thr	Ser	Gly	Val 345
Thr	Gln	Gly	Val	Val 350	Gly	Gly	Ala	Gly	Ala 355	Thr	Ala	Leu	Val	Phe 360
Leu	Ser	Phe	Cys	Val 365	Ile	Phe	Val	Val	Val 370	Arg	Ser	Cys	Arg	Lys 375
Lys	Ser	Ala	Arg	Pro 380	Ala	Ala	Gly	Val	Gly 385	Asp	Thr	Gly	Ile	Glu 390
Asp	Ala	Asn	Ala	Val 395	Arg	Gly	Ser	Ala	Ser 400	Gln	Gly	Pro	Leu	Thr 405



20					25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
				35					40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
				50					55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
				65					70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
				80					85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
				95					100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
				110					115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
				125					130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
				140					145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
				155					160					165
Cys	Val	Pro	Glu	His										
				170										

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-21  
 <223> Synthetic construct.

<400> 165  
 gtcctccgga aagtccttat c 21

<210> 166  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 166  
 gcctagtgtt cggaacgca gcttc 25

<210> 167  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 167  
 caggacctg gtacgtgaag gccatggtgg togataagga ctttccggag 50

<210> 168  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 168  
 ctgtccttca ccctggagga ggaggatata acaggacct ggtac 45

<210> 169  
 <211> 1204  
 <212> DNA  
 <213> Homo sapiens

<400> 169



gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50  
cagaggtctc acagcagcca aggaacctgg gggccgctcc tccccctcc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150  
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200  
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250  
cgacgctcat cggccccaga tggctcctga cagcagcca ctgcctcaag 300  
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350  
ctgtgagcag acccgagacag ccaactgagtc cttccccac cccggcttca 400  
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500  
ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
gcacgtccag ccccgagtta cgctgcctc acaccttgcg atgcgccaac 600  
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650  
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
attatctcct ggggccagga tccgtgtgag atcaccgaa agcctggtgt 800  
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cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000  
taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050  
ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100  
tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150  
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc ggggtg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca etc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcatcgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
 tgtgaccaa ggaccacgga gcattgagac atttaaacia atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcataatc aggatgcagt 600  
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
 ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750  
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850  
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
 aaaaaaa 907

<210> 180  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe  
 1 5 10 15  
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu  
 20 25 30  
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn  
 35 40 45  
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr  
 50 55 60  
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg  
 65 70 75  
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly  
 80 85 90  
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro  
 95 100 105  
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly  
 110 115 120  
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu  
 125 130 135  
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser  
 140 145 150



<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 184  
 gatgtctgcc accccaag 18

<210> 185  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 185  
 gcatcctgat atgacttgct acgtggc 27

<210> 186  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 186  
 tacaagaggg aagaggagtt gcac 24

<210> 187  
 <211> 52  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-52  
 <223> Synthetic construct.

<400> 187  
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
 cc 52

<210> 188  
 <211> 573  
 <212> DNA  
 <213> Homo sapiens

<400> 188  
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50  
 ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

cccaaagtgt tctgtgtca ataacactca ctgcacctgc aacctatgat 150  
 atactttctgg atctggggcag aaactattca cattccccctt ggagacatgt 200  
 aacgccaggc atggtgggtc gcgcctgtaa tcccagttct ttgggaagcc 250  
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggctggtt 350  
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
 ttcttgtttc atttcgcgac tgccctctca gtgttttctg ggatcccctc 550  
 ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15

Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30

Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45

Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60

Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu
				65					70				

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial



<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 191  
 cgttacatgt ctccaagggg aatg 24

<210> 192  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 192  
 cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193  
 <211> 1091  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
 caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
 ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
 gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150  
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
 gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
 gcctgcgctg cgggggtgtc ottattgacc acaggtgggt cctcacagcg 300  
 gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350  
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
 cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450  
 ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500  
 gccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
 gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
 cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700  
 atgcctgcca ggggtgattct gggggcccc tgggtgtgtgg gggagtcctt 750  
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccataccttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000  
 gccagccctt ctaagaccca cgagcggggg gagagaagtg tgcaatagtc 1050  
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
 gcggccacac gcagctagcc ggagccogga ccaggcgccct gtgcctcctc 50  
 ctcgctccctc gccgcgtccg cgaagcctgg agccggcgagg agccccgcgc 100  
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgctc 150  
 ggcttgctca aagcccgga ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350  
 caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400  
 tcagtgaacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450  
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500  
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550  
 tgccctgagg accccgctg gactccccag ccttcccacc ccatacctcc 600  
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650  
 tttgttttgt cattgagggt ttgttttgtt tttcatcaat gtctttgtaa 700  
 agcacaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750  
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800  
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850  
 cttccagcct gtgttcccc cacttgaggg aaccagcact ctccatcctt 900  
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950  
 gacccaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000  
 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

accaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
 attccacacc tcttctcatc ctcaagtatg tgaaggtggg aaggaaagga 1150  
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200  
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250  
 tactgtccct tactggggca gcagagggtc tcggaggcag aagtgaggcc 1300  
 tgggggtttg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350  
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgct 1450  
 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15

Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30

Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45

Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60

Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90

Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105

Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120

Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135

Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens



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attaccgcag	caggttcagc	agcgagtgct	tcattggacct	cgtgtgcccc	1600
gagaagtgtc	gctgtgaggg	cacgattgtg	gactgctcca	accagaagct	1650
ggtccgcata	ccaagccacc	tccctgaata	tgtcaccgac	ctgcgactga	1700
atgacaatga	ggtatctgtt	ctggaggcca	ctggcatctt	caagaagttg	1750
cccaacctgc	ggaaaataaa	tctgagtaac	aataagatca	aggagggtgcg	1800
agagggagct	ttcgatggag	cagccagcgt	gcaggagctg	atgctgacag	1850
ggaaccagct	ggagaccgtg	cacggggcgcg	tgttccgtgg	cctcagtggc	1900
ctcaaaacct	tgatgctgag	gagtaacttg	atcagctgtg	tgagtaatga	1950
cacctttgcc	ggcctgagtt	cggtgagact	gctgtccctc	tatgacaatc	2000
ggatcaccac	catcacccct	ggggccttca	ccacgcttgt	ctccctgtcc	2050
accataaacc	tctgtgtcaa	ccccttcaac	tgcaactgcc	acctggcctg	2100
gctcggcaag	tggttgagga	agaggcggat	cgtcagtggg	aacctaggt	2150
gccagaagcc	atttttcctc	aaggagattc	ccatccagga	tgtggccatc	2200
caggacttca	cctgtgatgg	caacgaggag	agtagctgcc	agctgagccc	2250
gcgctgcccgc	gagcagtgca	cctgtatgga	gacagtggtg	cgatgcagca	2300
acaaggggct	ccgcgcacctc	cccagaggca	tgcccaagga	tgtgaccgag	2350
ctgtacctgg	aaggaaacca	cctaacagcc	gtgccagag	agctgtccgc	2400
cctccgacac	ctgaocgtta	ttgacctgag	caacaacagc	atcagcatgc	2450
tgaccaatta	caccttcagt	aacatgtctc	acctctccac	tctgatcctg	2500
agctacaacc	ggctgaggtg	catccccgtc	cacgccttca	acgggctgcg	2550
gtccctgcga	gtgctaacc	tccatggcaa	tgacatttcc	agcgttcctg	2600
aaggctcctt	caacgacctc	acatctcttt	cccatctggc	gctgggaacc	2650
aacccaactcc	actgtgactg	cagtcttcgg	tggctgtcgg	agtgggtgaa	2700
ggcggggtac	aaggagcctg	gcacgcgccg	ctgcagtagc	cctgagccca	2750
tggctgacag	gtcctgtctc	accaccccaa	cccaccgctt	ccagtgcaaa	2800
gggccagtgg	acatcaacat	tgtggccaaa	tgcaatgcct	gcctctccag	2850
cccgctgcaag	aataacggga	catgcaccca	ggacctgtg	gagctgtacc	2900



catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagcg 4400  
 gcgagcactg ccaacaagag aatccgtgcc tgggacaagt agtccgagag 4450  
 gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500  
 gcccatcatg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550  
 cccgcagcaa gcggcggaaa tacgtcttcc agtgcacgga cggctcctcg 4600  
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 ctaagcccct gccgcctgc ctgccacctc toggactcca gcttgatgga 4700  
 gttgggacag ccatgtggga ccccctggtg attcagcatg aaggaaatga 4750  
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800  
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg
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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
				20					25					30
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
				35					40					45
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
				50					55					60
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
				65					70					75
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
				80					85					90
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
				95					100					105
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
				110					115					120
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
				125					130					135
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
				140					145					150
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
				155					160					165



Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	170	175	180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg	185	190	195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu	200	205	210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	215	220	225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr	230	235	240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp	245	250	255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro	260	265	270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr	275	280	285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu	290	295	300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu	305	310	315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr	320	325	330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	335	340	345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	350	355	360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	365	370	375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	380	385	390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	395	400	405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	410	415	420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	425	430	435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	440	445	450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser			

				455					460					465
Ser	Pro	Arg	Arg	Leu 470	Ala	Asn	Lys	Arg	Ile 475	Ser	Gln	Ile	Lys	Ser 480
Lys	Lys	Phe	Arg	Cys 485	Ser	Gly	Ser	Glu	Asp 490	Tyr	Arg	Ser	Arg	Phe 495
Ser	Ser	Glu	Cys	Phe 500	Met	Asp	Leu	Val	Cys 505	Pro	Glu	Lys	Cys	Arg 510
Cys	Glu	Gly	Thr	Ile 515	Val	Asp	Cys	Ser	Asn 520	Gln	Lys	Leu	Val	Arg 525
Ile	Pro	Ser	His	Leu 530	Pro	Glu	Tyr	Val	Thr 535	Asp	Leu	Arg	Leu	Asn 540
Asp	Asn	Glu	Val	Ser 545	Val	Leu	Glu	Ala	Thr 550	Gly	Ile	Phe	Lys	Lys 555
Leu	Pro	Asn	Leu	Arg 560	Lys	Ile	Asn	Leu	Ser 565	Asn	Asn	Lys	Ile	Lys 570
Glu	Val	Arg	Glu	Gly 575	Ala	Phe	Asp	Gly	Ala 580	Ala	Ser	Val	Gln	Glu 585
Leu	Met	Leu	Thr	Gly 590	Asn	Gln	Leu	Glu	Thr 595	Val	His	Gly	Arg	Val 600
Phe	Arg	Gly	Leu	Ser 605	Gly	Leu	Lys	Thr	Leu 610	Met	Leu	Arg	Ser	Asn 615
Leu	Ile	Ser	Cys	Val 620	Ser	Asn	Asp	Thr	Phe 625	Ala	Gly	Leu	Ser	Ser 630
Val	Arg	Leu	Leu	Ser 635	Leu	Tyr	Asp	Asn	Arg 640	Ile	Thr	Thr	Ile	Thr 645
Pro	Gly	Ala	Phe	Thr 650	Thr	Leu	Val	Ser	Leu 655	Ser	Thr	Ile	Asn	Leu 660
Leu	Ser	Asn	Pro	Phe 665	Asn	Cys	Asn	Cys	His 670	Leu	Ala	Trp	Leu	Gly 675
Lys	Trp	Leu	Arg	Lys 680	Arg	Arg	Ile	Val	Ser 685	Gly	Asn	Pro	Arg	Cys 690
Gln	Lys	Pro	Phe	Phe 695	Leu	Lys	Glu	Ile	Pro 700	Ile	Gln	Asp	Val	Ala 705
Ile	Gln	Asp	Phe	Thr 710	Cys	Asp	Gly	Asn	Glu 715	Glu	Ser	Ser	Cys	Gln 720
Leu	Ser	Pro	Arg	Cys 725	Pro	Glu	Gln	Cys	Thr 730	Cys	Met	Glu	Thr	Val 735
Val	Arg	Cys	Ser	Asn 740	Lys	Gly	Leu	Arg	Ala 745	Leu	Pro	Arg	Gly	Met 750

Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
				755					760					765	
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile	
				770					775					780	
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe	
				785					790					795	
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	
				800					805					810	
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu	
				815					820					825	
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu	
				830					835					840	
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly	
				845					850					855	
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu	
				860					865					870	
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser	
				875					880					885	
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr	
				890					895					900	
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala	
				905					910					915	
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr	
				920					925					930	
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr	
				935					940					945	
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile	
				950					955					960	
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser	
				965					970					975	
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly	
				980					985					990	
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	
				995					1000					1005	
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys	
				1010					1015					1020	
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile	
				1025					1030					1035	
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys	

				1040						1045					1050
Cys	Ile	Pro	Leu	Asp	Lys	Gly	Phe	Ser	Cys	Glu	Cys	Val	Pro	Gly	
				1055					1060					1065	
Tyr	Ser	Gly	Lys	Leu	Cys	Glu	Thr	Asp	Asn	Asp	Asp	Cys	Val	Ala	
				1070					1075					1080	
His	Lys	Cys	Arg	His	Gly	Ala	Gln	Cys	Val	Asp	Thr	Ile	Asn	Gly	
				1085					1090					1095	
Tyr	Thr	Cys	Thr	Cys	Pro	Gln	Gly	Phe	Ser	Gly	Pro	Phe	Cys	Glu	
				1100					1105					1110	
His	Pro	Pro	Pro	Met	Val	Leu	Leu	Gln	Thr	Ser	Pro	Cys	Asp	Gln	
				1115					1120					1125	
Tyr	Glu	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Val	Gln	Gln	Glu	
				1130					1135					1140	
Pro	Thr	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ala	Gly	Pro	Arg	Cys	Glu	
				1145					1150					1155	
Lys	Leu	Ile	Thr	Val	Asn	Phe	Val	Gly	Lys	Asp	Ser	Tyr	Val	Glu	
				1160					1165					1170	
Leu	Ala	Ser	Ala	Lys	Val	Arg	Pro	Gln	Ala	Asn	Ile	Ser	Leu	Gln	
				1175					1180					1185	
Val	Ala	Thr	Asp	Lys	Asp	Asn	Gly	Ile	Leu	Leu	Tyr	Lys	Gly	Asp	
				1190					1195					1200	
Asn	Asp	Pro	Leu	Ala	Leu	Glu	Leu	Tyr	Gln	Gly	His	Val	Arg	Leu	
				1205					1210					1215	
Val	Tyr	Asp	Ser	Leu	Ser	Ser	Pro	Pro	Thr	Thr	Val	Tyr	Ser	Val	
				1220					1225					1230	
Glu	Thr	Val	Asn	Asp	Gly	Gln	Phe	His	Ser	Val	Glu	Leu	Val	Thr	
				1235					1240					1245	
Leu	Asn	Gln	Thr	Leu	Asn	Leu	Val	Val	Asp	Lys	Gly	Thr	Pro	Lys	
				1250					1255					1260	
Ser	Leu	Gly	Lys	Leu	Gln	Lys	Gln	Pro	Ala	Val	Gly	Ile	Asn	Ser	
				1265					1270					1275	
Pro	Leu	Tyr	Leu	Gly	Gly	Ile	Pro	Thr	Ser	Thr	Gly	Leu	Ser	Ala	
				1280					1285					1290	
Leu	Arg	Gln	Gly	Thr	Asp	Arg	Pro	Leu	Gly	Gly	Phe	His	Gly	Cys	
				1295					1300					1305	
Ile	His	Glu	Val	Arg	Ile	Asn	Asn	Glu	Leu	Gln	Asp	Phe	Lys	Ala	
				1310					1315					1320	
Leu	Pro	Pro	Gln	Ser	Leu	Gly	Val	Ser	Pro	Gly	Cys	Lys	Ser	Cys	
				1325					1330					1335	

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser  
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
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<223> Synthetic construct.

<400> 200  
ttggttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcacgc tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150  
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600  
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccgt ttctcccaa tttccttctt caaacttgga 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750  
gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
   1                  5                  10                  15  
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
                   20                  25                  30  
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
                   35                  40                  45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
                   50                  55                  60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
                   65                  70                  75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
                   80                  85                  90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
                   95                  100                  105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
                   110                  115                  120  
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
                   125                  130                  135  
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
                   140                  145

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
ctcattggct gcctgggtcac aggc 24

<210> 206  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 206  
ccagtcggac aggtctctcc cctc 24

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 207  
tcagtgacca aggctgagca ggcg 24

<210> 208  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 208  
ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209  
<211> 1648  
<212> DNA  
<213> Homo sapiens

<400> 209  
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50  
cctcagcagt gtcattgtgt aaaaacgcc aagctgaatat atcatgcccc 100  
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250



agagagattc	tttttctaaa	cgactataca	gggcccgaat	tgactggata	300
gaggaatata	ccacaggcat	ggcagactgc	atcttagtca	acagccagtt	350
cacagctgct	gtttttaagg	aaacattcaa	gtccctgtct	cacatagacc	400
ctgatgtcct	ctatccatct	ctaaatgtca	ccagctttga	ctcagttggt	450
cctgaaaagc	tggatgacct	agtccccaag	gggaaaaaat	tcctgctgct	500
ctccatcaac	agatacgaaa	ggaagaaaaa	tctgactttg	gcactggaag	550
ccctagtaca	gctgogtgga	agattgacat	cccaagattg	ggagaggggt	600
catctgatcg	tggcaggtgg	ttatgacgag	agagtcctgg	agaatgtgga	650
acattatcag	gaattgaaga	aaatgggtcca	acagtccgac	cttggccagt	700
atgtgacctt	cttgaggtct	ttctcagaca	aacagaaaat	ctccctcctc	750
cacagctgca	cgtgtgtgct	ttacacacca	agcaatgagc	actttggcat	800
tgtccctctg	gaagccatgt	acatgcagtg	cccagtcatt	gctgttaatt	850
cgggtggacc	cttggagtoc	attgaccaca	gtgtcacagg	gtttctgtgt	900
gagcctgacc	cggtgcactt	ctcagaagca	atagaaaagt	tcatccgtga	950
accttcctta	aaagccaacca	tgggcctggc	tggaagagcc	agagtgaagg	1000
aaaaattttc	ccctgaagca	tttacagaac	agctctaccg	atatgttacc	1050
aaactgctgg	tataatcaga	ttgtttttta	gatctccatt	aatgtcattt	1100
ttatggattg	tagaccagtg	tttgaaacca	aaaaagaaac	ctagaatcta	1150
atgcagaaga	gatcttttta	aaaataaact	tgagtcttga	atgtgagcca	1200
ctttcctata	taccacacct	ccctgtccac	ttttcagaaa	aaccatgtct	1250
tttatgctat	aatcattoca	aattttgcca	gtgttaagtt	acaaatgtgg	1300
tgtcattcca	tgttcagcag	agtattttta	ttatattttc	tcgggattat	1350
tgctcttctg	tctataaatt	ttgaatgata	ctgtgcctta	attggttttc	1400
atagttttaag	tgtgtatcat	tatcaaagtt	gattaatttg	gcttcatagt	1450
ataatgagag	cagggctatt	gtagttccca	gattcaatcc	accgaagtgt	1500
tcactgtcat	ctgttaggga	atttttgttt	gtcctgtott	tgccctggatc	1550
catagcgaga	gtgctctgta	ttttttttta	gataatttgt	atttttgcac	1600
actgagatat	aataaaaggt	gtttatcata	aaaaaaaaaa	aaaaaaaaaa	1648

 $\langle 211 \rangle$  323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
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Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

1000517-100051

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg  
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg  
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr  
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val  
320

<210> 211  
<211> 1554  
<212> DNA  
<213> Homo sapiens

<400> 211  
gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50  
cttcgcgata ttccgcgtta ccttcttgct ggcgttggtg ggagccgtgc 100  
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
tttgcattgag ttctctggtta atttgcattga gagatatggg cctgtggtct 250  
ccttctggtt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300  
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400  
accacattgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600  
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
tgactcctta gtacaaggga accttaattga ccaacagatc ctagaagaca 850  
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
tgggcaatct gttttttaac cacctctgaa gaagttaaaa aaaaattata 950  
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
tggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200  
gatcgggttg atgatgaatt agtaatgaaa acttttttct cacttggatt 1250  
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cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
cattgttaaa ttgattgagg aaaacaacca ttttaaaaaa atctatgttg 1500  
aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
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Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala  
20 25 30

Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu  
35 40 45

Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn  
50 55 60

Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg  
65 70 75

Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His  
80 85 90

Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys  
95 100 105

Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn  
110 115 120

His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu  
125 130 135

Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

	140		145		150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser	155		160		165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val	170		175		180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln	185		190		195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu	200		205		210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu	215		220		225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys	230		235		240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser	245		250		255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser	260		265		270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys	275		280		285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys	290		295		300
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val	305		310		315
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu	320		325		330
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln	335		340		345
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg	350		355		360
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro	365		370		375
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp	380		385		390
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly	395		400		405
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr	410		415		420
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val	425		430		435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
 455 460

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
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 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100  
 tcagggcttg tgccctctcg cttcctgacg ctctgggcgc atctggtggt 150  
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
 gccgcgtct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtgca ctacgtattg gtacatTTTT gtcttctgca gtgcccttcc 450  
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600  
 ttccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750  
 aaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
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 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
 20 25 30  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
 35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
50 55 60  
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
65 70 75  
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
80 85 90  
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
95 100 105  
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
110 115 120  
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
125 130 135  
Lys Lys Lys Pro Phe  
140

<210> 215  
<211> 697  
<212> DNA  
<213> Homo sapiens

<400> 215  
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gaccgcgcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150  
ggcatcagag tgcgccagc acctgagcct gcccttaacg tatgtggtgg 200  
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
gtggctggaa cttcacgggt gccactcag gtcaattatg gaaccccatg 400  
tcattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450  
ccaggccatc cgggcagccc aggggtctact ggctgcgggt gtggctcagg 500  
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650  
catggccaaa aacccactg totccttctc caataaagat gtagctc 697

<210> 216  
<211> 196  
<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	
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Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	
			20						25					30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	
			35						40					45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	
			50						55					60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	
			65						70					75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	
			80						85					90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	
			95						100					105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	
			110						115					120	
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	
			125						130					135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	
			140						145					150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	
			155						160					165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	
			170						175					180	
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser	
			185						190					195	

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100

tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150

cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcgga 200





tcacctgtca gaccgggggtt ctcccggatc tggatggcgc cggcctctca 1700  
gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750  
tgttctgtgt gtctgtctgt ggggtggggg aggggagga agtcttgtga 1800  
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850  
aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200  
 gcgccgccgc cgccgtcgct cctgcagcgc tgtcgacctg gccgctagca 250  
 tcttcccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300  
 agcgccagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350  
 ccgggcgctg tccgcggtgc cggccgtgct gctggctctc acgctgccgg 400  
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
 aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500  
 ctcttctctc ccgctgggga tatcggtccg ggcgggccaac tccaaggtcg 550  
 ccttctcggc ggtgcgagc accaaccacg agccatccga gatgagcaac 600  
 aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650  
 tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
 tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750  
 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800  
 tgttactcgt gaagctgccg cgaatggtgt cctgctctac ctagataaag 850  
 aggataaggt ttacctaaaa ctggagaaag gtaatttggt tggaggctgg 900  
 cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950  
 ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000  
 gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
 ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
aagcagataa tacctatgct taaatgtaac agtcaaaaagc tgtctgcaag 1200  
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300  
gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgcca 1350  
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400  
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ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650  
aaagttgctt acccaaaatc taagtgtc atccctgagc ctcagcaaaa 1700  
cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750  
aatgattgat aataaccact ttattaaaaa cctaagggtt ttttttttct 1800  
cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850  
ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900  
tgccttaact ctttaaattg tatatattta tctgttttagc taatattaa 1950  
ttcaaataat ccatatctaa atttagtgca atatcttgtc ttttgtatag 2000  
gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050  
tatatgttaa aaaaa 2065

<210> 220  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 220  
Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu  
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Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp  
20 25 30  
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp  
35 40 45  
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 221  
 acggctcacc atgggctccg 20

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 222  
 aggaagagga gcccttgag tccg 24

<210> 223  
 <211> 40



<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
1				5					10					15	
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
				245					250					255	

Ser Arg

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226

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atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcgggtcga 100  
gagccatctg ggggttcttg ggcccaagaa cgtctcgcag aaagacgccg 150  
agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200  
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250  
gtctgtgaac gtcctgaaca agcagaaggg ggccgcttg ctgtttgttg 300  
tccgccagaa ggaggctgtg gtgtccttcc aggtgcccct aatcctgcga 350  
gggatgtttc agcgcaagta cctctaccaa aaagtggaa gaaccctgtg 400  
tcagcccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450  
tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500  
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550  
agcagcacag cccagttact tcaagtatga gttccctgaa ggctgggact 600  
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cctgccaga aagcggtcac cctcgagtcc tggtgatc ttttctggc 1100  
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ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350



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 aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttcct 1600  
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 cttgttggcc attggcatct gcaacctgct cctttacttc gccttctaca 2250  
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 aaagaattgc ccagctctg ggcaccctgg ccaccctggg ccttggatcc 3700  
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 ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850  
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 tgcattcaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 227  
 <211> 832  
 <212> PRT  
 <213> Homo sapiens

<400> 227  
 Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser  
 1 5 10 15  
 Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln  
 20 25 30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

	320		325		330
Ile Asp Arg Ala Cys	Pro Glu Ser Gly	His Pro Arg Val Leu	Ala		
335		340	345		
Asp Ser Phe Pro Gly	Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr	Gly		
350		355	360		
Ser Phe Glu Asn Val	Ser Gly Ser Thr	Asp Gly Leu Val Asp	Ser		
365		370	375		
Ala Gly Thr Gly Asp	Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser	Phe		
380		385	390		
Glu Pro Val Gly Thr	Arg Pro Arg Val	Asp Ser Met Ser Ser	Val		
395		400	405		
Glu Glu Asp Asp Tyr	Asp Thr Leu Thr	Asp Ile Asp Ser Asp	Lys		
410		415	420		
Asn Val Ile Arg Thr	Lys Gln Tyr Leu	Tyr Val Ala Asp Leu	Ala		
425		430	435		
Arg Lys Asp Lys Arg	Val Leu Arg Lys	Lys Tyr Gln Ile Tyr	Phe		
440		445	450		
Trp Asn Ile Ala Thr	Ile Ala Val Phe	Tyr Ala Leu Pro Val	Val		
455		460	465		
Gln Leu Val Ile Thr	Tyr Gln Thr Val	Val Asn Val Thr Gly	Asn		
470		475	480		
Gln Asp Ile Cys Tyr	Tyr Asn Phe Leu	Cys Ala His Pro Leu	Gly		
485		490	495		
Asn Leu Ser Ala Phe	Asn Asn Ile Leu	Ser Asn Leu Gly Tyr	Ile		
500		505	510		
Leu Leu Gly Leu Leu	Phe Leu Leu Ile	Ile Leu Gln Arg Glu	Ile		
515		520	525		
Asn His Asn Arg Ala	Leu Leu Arg Asn	Asp Leu Cys Ala Leu	Glu		
530		535	540		
Cys Gly Ile Pro Lys	His Phe Gly Leu	Phe Tyr Ala Met Gly	Thr		
545		550	555		
Ala Leu Met Met Glu	Gly Leu Leu Ser	Ala Cys Tyr His Val	Cys		
560		565	570		
Pro Asn Tyr Thr Asn	Phe Gln Phe Asp	Thr Ser Phe Met Tyr	Met		
575		580	585		
Ile Ala Gly Leu Cys	Met Leu Lys Leu	Tyr Gln Lys Arg His	Pro		
590		595	600		
Asp Ile Asn Ala Ser	Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala	Ile		
605		610	615		

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
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Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
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Arg	Asp	Lys	Ile	Tyr	Val	Phe									
				830											

<210> 228  
 <211> 2848  
 <212> DNA  
 <213> Homo sapiens

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 ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150  
 gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20					25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
			35						40					45
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
			50						55					60
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
			65						70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
			80						85					90
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val
			95						100					105
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn
			110						115					120
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu
			125						130					135
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala
			140						145					150
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe
			155						160					165
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe
			170						175					180
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly
			185						190					195
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu
			200						205					210
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala
			215						220					225
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser
			230						235					240
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro
			245						250					255
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr
			260						265					270
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu
			275						280					285
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala
			290						295					300
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp
			305						310					315



Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				335					340					345	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					375	
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
				440					445					450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455					460					465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470					475					480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
				485					490					495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
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Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
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His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560					565					570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
				575					580					585	
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590					595					600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

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Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp		
	620	625	630		
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu		
	635	640	645		
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His		
	650	655	660		
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser		
	665	670	675		
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val		
	680	685	690		
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr		
	695	700	705		
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile		
	710	715	720		
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val		
	725	730	735		
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg		
	740	745	750		
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val		
	755	760	765		
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile		
	770	775	780		
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp		
	785	790	795		
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val			
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 <213> Artificial

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<210> 231  
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 <213> Artificial Sequeunce

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 <222> full  
 <223> Synthetic oligonucleotide probe

<400> 231  
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<210> 232  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 232  
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<210> 233  
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 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
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 agctgcctct tgtttcattt cacctcagca cgtaccatct gtctttttgt 2650  
 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700  
 tcttaacctc ctgcctagga tttgtacagc atctgggtgtg tgcttataag 2750  
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	
				170					175					180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	
				185					190					195	
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	
				200					205					210	
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	
				215					220					225	
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	
				230					235					240	
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	
				245					250					255	
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	
				260					265					270	
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	
				275					280					285	
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	
				290					295					300	
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	
				305					310					315	
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	
				320					325					330	
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	
				335					340					345	
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	
				350					355					360	
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	
				365					370					375	
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
				380					385					390	
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	
				395					400					405	
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	
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Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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 ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
 cccgcccttc ctccacaaag agcaccctg cctcacagggt gtattccctc 200  
 aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250  
 gagtcagaac atcttcttct cccctgtgag tgtctocact tccctggcca 300  
 tgctctccct tggggccac tcagtcacca agaccagat tctccagggc 350  
 ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400  
 ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgaccttga 450  
 agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaaatt 500  
 ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550  
 tttctccaac ccctccattg cccaggcgag gatcaacagc catgtgaaaa 600  
 agaagacca agggaagggt gtagacataa tccaaggcct tgaccttctg 650  
 acggccatgg ttctggtgaa tcacattttc tttaaagcca agtgggagaa 700  
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 ttgacaaaaa tgctgatttt tctggaattg caaagagaga ctccctgcag 1100  
 gtttctaaag caaccacaa ggctgtgctg gatgtcagtg aagagggcac 1150  
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 gtccctctta cttcactgtc tccttcaata ggaccttcct gatgatgatt 1250  
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 cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350  
 tgcacaagaa ataacaacc acatccctct ttctgttctg aggggtgcatt 1400  
 tgacccagct ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

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 ggatgttgct gggttacat atttccattc cttggggctc ccaggaatgg 1600  
 aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataacac 1650  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
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 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
 35 40 45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
 50 55 60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
 65 70 75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
 80 85 90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
 95 100 105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
 110 115 120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
 125 130 135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
 140 145 150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
 155 160 165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
 170 175 180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
 185 190 195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

10000172.100001



				200					205					210
Lys	Trp	Glu	Lys	Pro 215	Phe	His	Leu	Glu	Tyr 220	Thr	Arg	Lys	Asn	Phe 225
Pro	Phe	Leu	Val	Gly 230	Glu	Gln	Val	Thr	Val 235	Gln	Val	Pro	Met	Met 240
His	Gln	Lys	Glu	Gln 245	Phe	Ala	Phe	Gly	Val 250	Asp	Thr	Glu	Leu	Asn 255
Cys	Phe	Val	Leu	Gln 260	Met	Asp	Tyr	Lys	Gly 265	Asp	Ala	Val	Ala	Phe 270
Phe	Val	Leu	Pro	Ser 275	Lys	Gly	Lys	Met	Arg 280	Gln	Leu	Glu	Gln	Ala 285
Leu	Ser	Ala	Arg	Thr 290	Leu	Ile	Lys	Trp	Ser 295	His	Ser	Leu	Gln	Lys 300
Arg	Trp	Ile	Glu	Val 305	Phe	Ile	Pro	Arg	Phe 310	Ser	Ile	Ser	Ala	Ser 315
Tyr	Asn	Leu	Glu	Thr 320	Ile	Leu	Pro	Lys	Met 325	Gly	Ile	Gln	Asn	Ala 330
Phe	Asp	Lys	Asn	Ala 335	Asp	Phe	Ser	Gly	Ile 340	Ala	Lys	Arg	Asp	Ser 345
Leu	Gln	Val	Ser	Lys 350	Ala	Thr	His	Lys	Ala 355	Val	Leu	Asp	Val	Ser 360
Glu	Glu	Gly	Thr	Glu 365	Ala	Thr	Ala	Ala	Thr 370	Thr	Thr	Lys	Phe	Ile 375
Val	Arg	Ser	Lys	Asp 380	Gly	Pro	Ser	Tyr	Phe 385	Thr	Val	Ser	Phe	Asn 390
Arg	Thr	Phe	Leu	Met 395	Met	Ile	Thr	Asn	Lys 400	Ala	Thr	Asp	Gly	Ile 405
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<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

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<210> 238



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 gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150  
 ctttctcaag aatcctctgt tctttgccct cttaaagtctt ggtacatcta 200  
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250  
 aaaggaaatg ttctccttat gtttggctta ctattgcatt tagaagctgc 300  
 aacaaattcc aatgagacta gcacctctgc caaacttga tccagtgtga 350  
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 agtggggcca gcacagccac catctcaggg tccagcgtga cctccaatgg 450  
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500  
 gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550  
 gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600  
 caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650  
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 ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950  
 gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000  
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 caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100  
 ctgagtccag cagcacctcc agtggggcca gcacagccac caactctgag 1150  
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 cacaacctcc agtggggcca gcacagccac caactctgag tccagcacag 1250  
 tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300  
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 ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400  
 gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450  
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Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				110					115					120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val
				125					130					135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				140					145					150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				155					160					165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				170					175					180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				185					190					195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				200					205					210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala
				215					220					225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				230					235					240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala
				245					250					255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				260					265					270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				275					280					285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				290					295					300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				305					310					315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala
				320					325					330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				335					340					345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				350					355					360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

	365		370		375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380		385		390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395		400		405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410		415		420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425		430		435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440		445		450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455		460		465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470		475		480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485		490		495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500		505		510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515		520		525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530		535		540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545		550		555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560		565		570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575		580		585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590		595		

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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 ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100  
 tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150  
 cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200  
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
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 gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500  
 ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550  
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 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
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 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900  
 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950  
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	
				20					25					30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	
				35					40					45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	
				50					55					60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	
				65					70					75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	
				80					85					90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	
				95					100					105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	
				110					115					120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	
				125					130					135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	
				140					145					150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	
				155					160					165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	
				170					175					180	



Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly  
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
230 235 240

Ser Val Ala Asn Ile Met Pro  
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatc ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

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tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcgacc gcggggcgga gctgcggccc gtgagtcgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcga 250
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300
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Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
				710										720					
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
				725										735					
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
				740										750					
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
				755										765					
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
				770										780					
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
				785										795					
Asn	Gly	Ser	Val	Arg	Thr	Ala													
				800															

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<212> DNA  
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<220>  
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<222> 1-24  
<223> Synthetic construct.

<400> 261  
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<210> 262  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 262  
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<210> 263  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 263  
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<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
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tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccaccattc 500  
 tggtcgatca aaccaaacia tgtttccatt gttttgcatg cagaggaacc 550  
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaac 600  
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650  
 ccatatgtta cctcatacaa gtcacctgtc accacttttag ataagagcac 700  
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750  
 aaactgcatg agaaaaacc gaagagtttg gaaagcacc agagagttgg 800  
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 acaggcactt cttagtgcac ccagcaaccc agcatataga gaagatattg 900  
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 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050  
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 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser



				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly
				95					100					105
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro
				110					115					120
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala
				125					130					135
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu
				140					145					150
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val
				155					160					165
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro
				170					175					180
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu
				185					190					195
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys
				200					205					210
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp
				215					220					225
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala
				230					235					240
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu
				245					250					255
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala
				260					265					270
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro
				275					280					285
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile
				290					295					300
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp
				305					310					315
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val
				320					325					330
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala
				335					340					345



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ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300
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caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
ttgttgagac cctatatcca gcatgcatg tatgacgagg aaaaggggac 1500
tcccatattc atatgtccag tgcctggggg atgagacaga gaagaccctg 1550
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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
  1             5             10             15

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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

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	20	25	30
Leu Val Gly Glu Asp	Ala Val Phe Ser	Cys Ser Leu Phe Pro	Glu
	35	40	45
Thr Ser Ala Glu Ala	Met Glu Val Arg	Phe Phe Arg Asn Gln	Phe
	50	55	60
His Ala Val Val His	Leu Tyr Arg Asp	Gly Glu Asp Trp Glu	Ser
	65	70	75
Lys Gln Met Pro Gln	Tyr Arg Gly Arg	Thr Glu Phe Val Lys	Asp
	80	85	90
Ser Ile Ala Gly Gly	Arg Val Ser Leu	Arg Leu Lys Asn Ile	Thr
	95	100	105
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys	Trp Phe Ser Ser Gln	Ile
	110	115	120
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu	Arg Val Ala Ala Leu	Gly
	125	130	135
Ser Leu Pro Leu Ile	Ser Ile Val Gly	Tyr Val Asp Gly Gly	Ile
	140	145	150
Gln Leu Leu Cys Leu	Ser Ser Gly Trp	Phe Pro Gln Pro Thr	Ala
	155	160	165
Lys Trp Lys Gly Pro	Gln Gly Gln Asp	Leu Ser Ser Asp Ser	Arg
	170	175	180
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr	Asp Val Glu Ile Ser	Ile
	185	190	195
Ile Val Gln Glu Asn	Ala Gly Ser Ile	Leu Cys Ser Ile His	Leu
	200	205	210
Ala Glu Gln Ser His	Glu Val Glu Ser	Lys Val Leu Ile Gly	Glu
	215	220	225
Thr Phe Phe Gln Pro	Ser Pro Trp Arg	Leu Ala Ser Ile Leu	Leu
	230	235	240
Gly Leu Leu Cys Gly	Ala Leu Cys Gly	Val Val Met Gly Met	Ile
	245	250	255
Ile Val Phe Phe Lys	Ser Lys Gly Lys	Ile Gln Ala Glu Leu	Asp
	260	265	270
Trp Arg Arg Lys His	Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys
	275	280	285
His Ala Val Glu Val	Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys
	290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val	Thr His Arg Lys Ala	Pro
	305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 gtcattctca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150  
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
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 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
 agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450  
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500



atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000  
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050  
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100  
 cca 2103

<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269  
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
 35 40 45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
 50 55 60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
 65 70 75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
 80 85 90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
 95 100 105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
 110 115 120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
 125 130 135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
 140 145 150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
 155 160 165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
 170 175 180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
 185 190 195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
 200 205 210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
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Thr Gly Ile

<210> 270  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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			20					25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40						45
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
			50					55						60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
			65					70						75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
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Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
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<210> 272  
 <211> 2397  
 <212> DNA  
 <213> Homo sapiens

<400> 272  
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 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200  
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250  
 acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300  
 tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350  
 aacgagggta gaggaagcag tcattttgac ttactttcct gtgggttcac 400  
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aagtttgctt gtcattttct gtgtagaact ggcttggtgc gtttggacat 550  
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg 600  
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tgcttggaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700  
tcactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750  
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Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His	Gln		
	185		190		195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met		
	200		205		210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe		
	215		220		225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu		
	230		235		240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu	Pro		
	245		250		255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His		
	260		265		270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg		
	275		280		285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His	Phe		
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<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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tggactgtcc cttggggggag gacgaggagc actgtgtcaa gagcttcccc 500

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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg  
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser  
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr  
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln  
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu  
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg  
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr  
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu  
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu  
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn  
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser  
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu  
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser  
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys  
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His  
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala  
245 250 255

265

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

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Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
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Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
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<210> 278  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 278  
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<210> 279  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.



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<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly



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275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial



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tgggggcccgg	gtgggcccag	gaggggtcag	agcccgctct	gctggagggg	600
gagtgcctgg	tggctctgtga	gcctggccga	gctgctgcag	gggggcccgg	650
gggagcagcc	ctgggagagg	cacccccctgg	gcgagtggca	tttgctgcgg	700
tccgaagcca	ccaccatgag	ccagcagggg	aaaccggcaa	tggcaccagt	750
ggggccatct	acttcgacca	ggtcctgggtg	aacgagggcg	gtggctttga	800
ccggggcctct	ggctccttcg	tagccccctgt	ccgggggtgtc	tacagcttcc	850
ggttccatgt	ggtgaagggtg	tacaaccgcc	aaactgtcca	ggtgagcctg	900
atgctgaaca	cgtggcctgt	catctcagcc	tttgccaatg	atcctgacgt	950
gacccgggag	gcagccacca	gctctgtgct	actgcccttg	gaccctgggg	1000
accgagtgtc	tctgcgcctg	cgtcggggga	atctactggg	tggttggaaa	1050
tactcaagtt	tctctggctt	cctcatcttc	cctctctgag	gacccaagtc	1100
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 caactagaga atgggtggtca gtgagacact atagaattac taaggagaag 2250  
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170	175	180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser			
	185	190	195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu			
	200	205	

<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
 aggcagccac cagctctgtg ctac 24

<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
 cagagaggga agatgaggaa gccagag 27

<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
 ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 gctgtttctc tcggccacc actggccgcc ggccgcagct ccaggtgtcc 50  
 tagccgcccc gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100  
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg	gccgtgactg	ggcgggcttc	agccatgaag	accctcatag	200
ccgcctactc	cgggggtcctg	cgcggcgagc	gtcaggccga	ggctgaccgg	250
agccagcgct	ctcacggagg	acctgcgctg	tcgcgcgagg	ggctctgggag	300
atggggcact	ggatccagca	tcctctccgc	cctccaggac	ctctttctctg	350
tcacctggct	caataggtcc	aaggtggaaa	agcagctaca	ggtcattctca	400
gtgctccagt	gggtcctgtc	cttccttgta	ctgggagtgg	cctgcagtgc	450
catcctcatg	tacatatctt	gcactgattg	ctggctcatc	gctgtgctct	500
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tttgctctgt	aaatttgga	gtgtcatggg	tgtctgtggg	ttatttaaaa	1450
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1550
aaaaaaaaaa	aaaaaaaaaa	1570			

<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				





<221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 295  
 aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296  
 <211> 3060  
 <212> DNA  
 <213> Homo sapiens

<400> 296  
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 ccgacgcagg gccggggccg gccagggcc gaggagcgcg gcggccagag 100  
 cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150  
 gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
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 cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
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 ccagggagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000  
 cagtgaagtcg aggttgtgctg actgcattcc agcctggaca acagagtgcg 3050  
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro	Glu	Tyr	Met	Trp 170	Phe	Leu	Leu	Tyr	Cys 175	Glu	Gly	Thr	Arg		Phe 180
Thr	Glu	Thr	Lys	His 185	Arg	Val	Ser	Met	Glu 190	Val	Ala	Ala	Ala		Lys 195
Gly	Leu	Pro	Val	Leu 200	Lys	Tyr	His	Leu	Leu 205	Pro	Arg	Thr	Lys		Gly 210
Phe	Thr	Thr	Ala	Val 215	Lys	Cys	Leu	Arg	Gly 220	Thr	Val	Ala	Ala		Val 225
Tyr	Asp	Val	Thr	Leu 230	Asn	Phe	Arg	Gly	Asn 235	Lys	Asn	Pro	Ser		Leu 240
Leu	Gly	Ile	Leu	Tyr 245	Gly	Lys	Lys	Tyr	Glu 250	Ala	Asp	Met	Cys		Val 255
Arg	Arg	Phe	Pro	Leu 260	Glu	Asp	Ile	Pro	Leu 265	Asp	Glu	Lys	Glu		Ala 270
Ala	Gln	Trp	Leu	His 275	Lys	Leu	Tyr	Gln	Glu 280	Lys	Asp	Ala	Leu		Gln 285
Glu	Ile	Tyr	Asn	Gln 290	Lys	Gly	Met	Phe	Pro 295	Gly	Glu	Gln	Phe		Lys 300
Pro	Ala	Arg	Arg	Pro 305	Trp	Thr	Leu	Leu	Asn 310	Phe	Leu	Ser	Trp		Ala 315
Thr	Ile	Leu	Leu	Ser 320	Pro	Leu	Phe	Ser	Phe 325	Val	Leu	Gly	Val		Phe 330
Ala	Ser	Gly	Ser	Pro 335	Leu	Leu	Ile	Leu	Thr 340	Phe	Leu	Gly	Phe		Val 345
Gly	Ala	Ala	Ser	Phe 350	Gly	Val	Arg	Arg	Leu 355	Ile	Gly	Glu	Ser		Leu 360
Glu	Pro	Gly	Arg	Trp 365	Arg	Leu	Gln								

<210> 298

<211> 24

<212> DNA

<213> Artificial

 $\langle 220 \rangle$ 

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtaggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

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<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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gttgtatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750









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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
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Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
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Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
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Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
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Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
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Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
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Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
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Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
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Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
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Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
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Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
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 <212> DNA  
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<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
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Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

				140					145					150
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser
				155					160					165
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala
				170					175					180
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu
				185					190					195
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala
				200					205					210
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys
				215					220					225
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser
				230					235					240
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser
				245					250					255
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val
				260					265					270
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro
				275					280					285
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser
				290					295					300
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu
				305					310					315
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg
				320					325					330
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
				335					340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly
				350					355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg
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Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly
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Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
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Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser
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Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
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Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	
				455					460					465	
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Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
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Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
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				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
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Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
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Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
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Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
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Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
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Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
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<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45
Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
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Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75
Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile

				80					85					90
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
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Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
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Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
				230					235					240
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu
				260					265					270
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
				275					280					285
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
				290					295					300
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser
				305					310					315
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu
				320					325					330
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
				335					340					345
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
				350					355					360
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His
				365					370					375

Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	380	385	390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	515	520	525
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	530	535	540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	545	550	555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	560	565	570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu	
680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu	
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu	
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp	
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp	
740	745	750
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His	
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr	
770	775	

<210> 311  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 311  
 caacgcagcc gtgataaaca agtgg 25

<210> 312  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 312  
 gcttggacat gtaccaggcc gtgg 24

<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.



gacctctccc tcccagagag cagccaagac agtgacaatc cctgcggggc 1300  
 agagcccaca gcattccttg cacaggccct gtacagctac accggacaga 1350  
 gtgcagagga gctgagcttc cctgaggggg cactcatccg tctgctgccc 1400  
 cgggcccagg atggagtaga tgacggcttc tggaggggag aatttggggg 1450  
 ccgtgttggg gtcttccctt ccctgctggt ggaagagctg cttggcccc 1500  
 cagggccacc tgaactctct gacctgaac agatgctgcc gtccccctct 1550  
 cctcccagct tctcccacc tgcacctacc tctgtgttg atgggcccc 1600  
 tgcacctgtc ctgcctgggg acaaagccct ggacttccct gggttcctgg 1650  
 acatgatggc acctcgactc aggccgatgc gtccaccacc tccccgcgcg 1700  
 gctaaagccc cggatccttg ccaccagat cccctcacct gaaggccagg 1750  
 gaagccttga ccccagtg tgctgctgtc cctatcttca agctgtcaga 1800  
 ccacaccatc aatgatccag agcaacacag ccaaaagctg gaatcgccct 1850  
 tatttccacc ctacactcca agggtggaat cttgcccctt cccatttcta 1900  
 gagctggaac cactccttt tttccctatt gttctatcat ctctaggacc 1950  
 ggaactacta ccttctcttc tgtcatgacc ctatctaggg tggtgaaatg 2000  
 cctgaaatct ctggggcttg aaaccatcca tcaaggtctc tagtagttct 2050  
 ggccacctc tttcccacc ctggctccat gaccacccc actctggatg 2100  
 ccagggtcac tgggggttgg ctggggagag gaacaggcct tgggaatcag 2150  
 gagctggagc caggatgcga agcagctgta atggtctgag cggatttatt 2200  
 gacaatgaat aaagggcacg aaggccaggc cagggcctgg gcctcttctg 2250  
 ctaagagggc agggggccta cgggtctatt gctttagggg cccaccacgg 2300  
 gcaggggctt gctcccagct gccacgtct atcatatgga gcgagggtgt 2350  
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 tgaggggctg tgacctctcc tgaggcccc agcctgagac tgtgcaactc 2450  
 cagggtggaag tagagctggt ccctcagctg gggggcagtg ctgtccagtg 2500  
 gaggggaggg ctttcacgcc caccacccc ctggccctgc cagctggtag 2550  
 tccatcagca caatgaagga gacttgaga agaggaagaa taactgtt 2600  
 gcttctgtt caagctgtgt ccagcttttc ccctggggct ccaggacctt 2650  
 ccctacctcc accaccaaac caagggattt atagcaaagg ctaagcctgc 2700



Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu	20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala			



305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro Gly	
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro	
335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys Ala	
350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
365	370	

<210> 316  
 <211> 4407  
 <212> DNA  
 <213> Homo sapiens

<400> 316  
 cacagggaga cccacagaca catatgcacg agagagacag aggaggaaag 50  
 agacagagac aaaggcacag cggaagaagg cagagacagg gcaggcacag 100  
 aagcggccca gacagagtcc tacagaggga gaggccagag aagctgcaga 150  
 agacacaggc agggagagac aaagatccag gaaaggaggg ctcaggagga 200  
 gagtttgag aagccagacc cctgggcacc tctcccaagc ccaaggacta 250  
 agttttctcc atttccttta acggtcctca gcccttctga aaactttgcc 300  
 tctgaccttg gcaggagtcc aagccccag gctacagaga ggagctttcc 350  
 aaagctaggg tgtggaggac ttggtgccct agacggcctc agtccctccc 400  
 agctgcagta ccagtgccat gtcccagaca ggctcgcac cggggagggg 450  
 cttggcaggg cgctggctgt ggggagccca accctgcctc ctgctcccca 500  
 ttgtgccgct ctctggctg gtgtggctgc ttctgctact gctggcctct 550  
 ctctgccct cagcccggct ggccagcccc ctccccggg aggaggagat 600  
 cgtgtttcca gagaagctca acggcagcgt cctgcctggc tcgggcgccc 650  
 ctgccaggct gttgtgccgc ttgcaggcct ttggggagac gctgctacta 700  
 gagctggagc aggactccgg tgtgcaggtc gaggggctga cagtgcagta 750  
 cctgggccag gcgcctgagc tgctgggtgg agcagagcct ggcacctacc 800  
 tgactggcac catcaatga gatccggagt cgggtggcatc tctgactgg 850  
 gatgggggag ccctgttagg cgtgttaca tatcgggggg ctgaactcca 900  
 cctccagccc ctggaggag gcacccctaa ctctgctggg ggacctggg 950





accaccacgc ccggctaatt tttgtatatt tagtagagac ggggtttcac 3900  
catgttggcc aggctggtct cgaactcctg accttaggtg atccactcgc 3950  
cttcatctcc caaagtgctg ggattacagg cgtgagccac cgtgcctggc 4000  
cacgccaac taatTTTTgt atttttagta gagacaggggt ttcaccatgt 4050  
tggccaggct gctcttgaac tcctgacctc aggtaatcga cctgcctcgg 4100  
cctcccaaag tgctgggatt acaggtgtga gccaccacgc ccggtacata 4150  
ttttttaaat tgaattctac tatttatgtg atccttttgg agtcagacag 4200  
atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250  
ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300  
aataaagaac tagcataaca ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400  
aaggaaa 4407

<210> 317  
<211> 837  
<212> PRT  
<213> Homo sapiens

<400> 317  
Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg  
1 5 10 15  
Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro  
20 25 30  
Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu  
35 40 45  
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu  
50 55 60  
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser  
65 70 75  
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu  
80 85 90  
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu  
95 100 105  
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly  
110 115 120  
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp  
125 130 135  
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

				140					145					150
Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
				155					160					165
Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
				170					175					180
Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
				185					190					195
Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
				200					205					210
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
				215					220					225
Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
				230					235					240
Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
				245					250					255
Pro	Ser	Ile	Arg	Asn	Pro	Val	Ser	Leu	Val	Val	Thr	Arg	Leu	Val
				260					265					270
Ile	Leu	Gly	Ser	Gly	Glu	Glu	Gly	Pro	Gln	Val	Gly	Pro	Ser	Ala
				275					280					285
Ala	Gln	Thr	Leu	Arg	Ser	Phe	Cys	Ala	Trp	Gln	Arg	Gly	Leu	Asn
				290					295					300
Thr	Pro	Glu	Asp	Ser	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu
				305					310					315
Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	Leu
				320					325					330
Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys
				335					340					345
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala
				350					355					360
His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys
				365					370					375
Pro	Cys	Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val
				380					385					390
Met	Ala	Pro	Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser
				395					400					405
Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr
				410					415					420
Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro
				425					430					435

Val	Thr	Phe	Pro	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln	440	445	450
Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro	455	460	465
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala	470	475	480
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys	485	490	495
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp	500	505	510
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro	515	520	525
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	530	535	540
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly	545	550	555
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn	560	565	570
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu	575	580	585
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe	590	595	600
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro	605	610	615
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr	620	625	630
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser	635	640	645
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala	650	655	660
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys	665	670	675
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly	680	685	690
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile	695	700	705
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro	710	715	720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser			

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
 ccctgaagct gccagatggc tcc 23

<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctctt cggtgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.





<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	1	5	10	15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	





Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
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 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccgggt 150  
 gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 200  
 aaccccgctca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250  
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300  
 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350  
 gtccctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400  
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450  
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500  
 gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat 550  
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 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
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 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050  
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 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
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tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
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 cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450  
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 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
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 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
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<210> 326  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
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 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp  
 20 25 30  
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln  
 35 40 45  
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe  
 50 55 60  
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met  
 65 70 75  
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe 95	Ala Leu Lys Cys Ile Arg 100	
Ile Gly Ser Met Glu Asp Ser Ala Lys 110	Ala Asn Met Thr Leu Thr 115	
Ser Gly Ile Met Phe Ile Val Ser Gly 125	Leu Cys Ala Ile Ala Gly 130	
Val Ser Val Phe Ala Asn Met Leu Val 140	Thr Asn Phe Trp Met Ser 145	
Thr Ala Asn Met Tyr Thr Gly Met Gly 155	Gly Met Val Gln Thr Val 160	
Gln Thr Arg Tyr Thr Phe Gly Ala Ala 170	Leu Phe Val Gly Trp Val 175	
Ala Gly Gly Leu Thr Leu Ile Gly Gly 185	Val Met Met Cys Ile Ala 190	
Cys Arg Gly Leu Ala Pro Glu Glu Thr 200	Asn Tyr Lys Ala Val Ser 205	
Tyr His Ala Ser Gly His Ser Val Ala 215	Tyr Lys Pro Gly Gly Phe 220	
Lys Ala Ser Thr Gly Phe Gly Ser Asn 230	Thr Lys Asn Lys Lys Ile 235	
Tyr Asp Gly Gly Ala Arg Thr Glu Asp 245	Glu Val Gln Ser Tyr Pro 250	
Ser Lys His Asp Tyr Val 260		

<210> 327  
 <211> 2010  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
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 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200  
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250  
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300  
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350







Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
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<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

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 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150  
 gcctgtggat gtctgctgtg gtgcagagca ccggccagat gcagtgcaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
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 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
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 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500  
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 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650  
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700  
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750  
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 agagttcctg ctgctgctgg gggctgggct tccctagatg tctactggaca 1050  
 gctgcccccc atcctactca ggtctctgga gctcctctct tacccttg 1100  
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150  
 cctctgtttc ctccgtctg ataagacgtc cccccccag ggccaggtcc 1200  
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgcct 1250

1000bp = 1000000

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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA



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Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250

gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300

aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350

tcatcatccc aggtcttgac tgagtttctt tcagttttac tgatgttctg 400

ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaaagt 450





agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300  
 ccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350  
 gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400  
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450  
 cccacgacac cattggctcc ttgaaaagga ccagtttcc cggccgggaa 500  
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 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650  
 cccggccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700  
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750  
 ttcccctgac cgccactctg ggccctggccg gcttcaccct gtcctcagt 800  
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 acgccaggtc ggtgggaggc tggtgaaggg gagcggggag gggcagagga 1250  
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaa 1300  
 aaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
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Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30

Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45





aggacttgga tgggtttgag gggtactccc tgagtgactg gctgtgcctg 300  
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400  
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
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gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550  
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ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750  
tcttggtctc ctccttactc ccatctggac ccagtcccct gggtcctgtc 800  
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

<210> 341  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 341  
 ccctccaagg atgacaaagg cgc 23

<210> 342  
 <211> 29  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-29  
 <223> Synthetic construct.

<400> 342  
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 343  
 atctcaggcg gcacacctgac agcc 24

<210> 344  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 344  
 gtggatgcct gcaagaaggt tggg 24

<210> 345  
 <211> 45  
 <212> DNA  
 <213> Artificial



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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 350  
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45





ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350  
ggcagctgtg gggagctggg gccacagggg ctcttggtct ctgccccttg 1400  
cacaccaccc ggaacactcc ccagcccac gggcaatcct atctgtctgc 1450  
cctcctgcag gtgggggcct cacatatctg tgacttcggg tccctgtccc 1500  
cacccttggt cactcacatg aaagccttgc aactcacct ccaccttcac 1550  
aggccatttg cacacgtcc tgcaccctct ccccgctcat accgctccgc 1600  
tcagctgact ctcatgttct ctgctctcac atttgcactc tctccttccc 1650  
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gctgctccag aggtgggtgg gaggtgagct gggggctcct tgggccctca 1850  
tcggtcatgg tctcgtccca ttccacacca tttgtttctc tgtctcccca 1900  
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tctgacagat gggttttggg gagtcgcctg ctgcactaca tgagaaaggg 2050  
actcccattt gcccttccct ttctcctaca gtcccttttg tcttgtctgt 2100  
cctggctgtc tgtgtgtgtg ccattctctg gacttcagag cccctgagc 2150  
cagtcctccc ttcccagcct ccctttgggc ctccctaact ccacctaggc 2200  
tgccagggac cggagtcagc tggttcaagg ccacgggag ctctgcctcc 2250  
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tcaaataaag cctttgcaag ataa 2524

<210> 352  
<211> 243  
<212> PRT  
<213> Homo sapiens

<400> 352  
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
 20 25 30  
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135  
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
 140 145 150  
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
 155 160 165  
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
 170 175 180  
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
 185 190 195  
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
 200 205 210  
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
 215 220 225  
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
 230 235 240

Leu Pro Lys

<210> 353  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 353  
 gttaccagc gcagtcctcc gtgcgtcccg cccgcgctg ccctcactcc 50  
 cggccaggat ggcacccgtg ctggccctgc gcatggcgct gctgctggtc 100



gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150  
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtctctgg 200  
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400  
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcagctgg ggaggaggcg agctctccag ggagggaccc 500  
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
agtagccccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600  
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggccc 650  
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750  
acgtcgcttg ctttggctat aactgcgagt agggctcagg catcacacc 800  
acctgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850  
gggctccccg cttccacct ggctgtcatc gggtagggcg gggcgtggg 900  
ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctggcgcgag 950  
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000  
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100  
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cgggcatctt tcctaaaggg tccccatagg gtctggttcc acccatccc 1250  
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ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350  
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400  
agaggagggg ggctagggg tcctctagat cagtgggggc actgcaggtg 1450  
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acctatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600  
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 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
 gctgggcctg ccccaggga acgtgggggc ggagactcag ctggacagcc 1950  
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 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050  
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 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
 125 130 135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro  
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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cctcttattt ctctctacgt gtgagctggc tgcagaagtt gctgcagaag 100  
ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc caogtggctc 150  
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
cataggcttc ttccaggatt tagaaatacc agcagtgtccc atactccata 250  
gcatgggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300  
gaggttctga cactactaca catcactggg aacaccatct gcctctttcg 350  
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400  
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450  
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
tcagattcat ctctctctga taatgaacaa ggctcccca gagtatgaag 550  
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
ctctttattc tgggtggacag tggatatgaa gaaaatggga aggtgatatc 650  
atctttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700  
ctctagatga cgagtgggat aactgtccca cagcagaagt ttccgtagag 750  
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800  
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850  
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
aactcaaate tcagagacac taaacaacag gatcactagg cctgccaacc 950  
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000  
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100  
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200



Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 359  
 ccagcagtgc ccatactcca tagc 24  
  
 <210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.  
  
 <400> 360  
 tgacgagtgg gatacactgc 20  
  
 <210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 361  
 gctctacgga aacttctgct gtgg 24  
  
 <210> 362



<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50  
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagcaa 100  
cctcagcggg gaccgggct cagggacgcg gcggcgggcg cggcgactgc 150  
agtggctgga cgatggcagc gtccgcgga gccggggcg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggg gctggcgggc gcgcttgggc 250  
tcttgacagc tggagtatca gccttgaag tatatacgcc aaaagaaatc 300  
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcgggttga cctcagtcct ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
cttggggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550  
atggcaccta tatctgtgat gtcaaaaacc ctcctgacat cgttgtccag 600  
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgcctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900  
tccggcgagc atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

10005172.10001

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ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200  
atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
ccttttaatc taagggtta agactgatta gtcttagcat ttactgtagt 1400  
tggaggatgg agatgctatg atggaagcat acccaggggt gccttttagca 1450  
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ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
tttgaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
attagcaaag gataaatgcc gaaggctcact tcattctgga cacagttgga 1700  
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364  
<211> 269  
<212> PRT  
<213> Homo sapiens

<400> 364  
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp  
1 5 10 15  
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
20 25 30  
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
35 40 45  
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
50 55 60  
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
65 70 75  
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
80 85 90  
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
95 100 105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
				110					115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
				125					130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
				140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
				155					160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
				170					175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
				185					190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				200					205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
				215					220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
				230					235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
				245					250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
				260					265					

<210> 365  
 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
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 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100  
 ccatcagcgc gccgggtgc cgcctctcgg ccacggctgg gtcgggggccc 150  
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200  
 aggggcgcgg ccccggcga gtccccgcg gccccgacc ctgaggcgtc 250  
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300  
 agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350  
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400  
 agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450  
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggtttc tgtcacaaca 650  
 agattactga tttcccatTT aagtgggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcTTataa agccttgaag atgatgaaag 750  
 agaatgtttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000  
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050  
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaaggT aatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250  
 gagcttttct acatgtctgt tttctcatct gttaaagtga ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15

Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65					70					75

Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80					85					90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			365	370	

<210> 367

<211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-30  
 <223> Synthetic construct.

<400> 367  
 tggaaaagaa gtctgggtcag aaggtttagg 30

<210> 368  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 368  
 catttggctt cattctcctg ctctg 25

<210> 369  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 369  
 aaaacctcag aacaactcat ttgcacc 28

<210> 370  
 <211> 41  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-41  
 <223> Synthetic construct.

<400> 370  
 gtctcacat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371  
 <211> 1150  
 <212> DNA  
 <213> Homo sapiens

<400> 371  
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150  
agtcgagccc ggggcagcgg ctgccgggcc gggactgggt gcgaggggc 200  
tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250  
tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300  
tactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350  
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
gaagctgggt gctatgtctc ctcccttgtc cctgcgtgct ccctggtgga 500  
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600  
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650  
gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgccctg 700  
agatggaaca ggcccagaag gccagaacc cccaggagca gaagtccttc 750  
ttcgccaaat actggatgta catcattccc gtctcctgt tcctcatgat 800  
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
agcttcacg agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000  
tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35				40						45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150

tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200





ctctgtgtta ctccattta gaaaataaac acttttaaata gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

10005176-1000501

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375  
 <211> 1098  
 <212> DNA  
 <213> Artificial

<400> 375  
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50  
 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctotg 100  
 gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaaagg actttggtgg tatctttcac acaaggatatg agcagattca 250



Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln  
95 100 105  
Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp  
110 115 120  
Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg  
125 130 135  
Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr  
140 145 150  
Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile  
155 160 165  
Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu  
170 175 180  
Leu Gln Pro Pro Trp Thr Phe Trp  
185

<210> 377  
<211> 496  
<212> DNA  
<213> Artificial

<220>  
<221> unsure  
<222> 396  
<223> unknown base

<400> 377  
tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150  
ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
aagaccagc ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300  
ttgtatgat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
<211> 116  
<212> PRT  
<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35					40						45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50					55						60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65					70						75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80					85						90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95					100						105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110					115						

<210> 379  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 379  
 ctgcctccac tgctctgtgc tggg 24

<210> 380  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 380  
 cagagcagtg gatgttcccc tggg 24

<210> 381  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt cctttctggat gggggcccag gggggcccagg agagtataaa 50  
 ggcgatgtgg aggggtgccg gcacaaccag acgcccagtc acaggcgaga 100  
 gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
 ctctgggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200  
 caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
 ggggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300  
 gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
 caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
 ctttcctccg gggtatggtc atgtacacca gcaaggaccg ctatttctat 450  
 tttgggaagc ttgatggcca gatctcctct gcctaccca gccaaaggagg 500  
 gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550  
 gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
 ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650  
 ggtatggggc catccgagct gaggccatct gtgtgggtgg ggctgatggt 700  
 actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
 gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1					5				10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50  
 agctctgtgg ctgaactggg tgctcatcac ggggaactgct gggctatgga 100  
 atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150  
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
 tggtgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttctctggg 400  
 tgtcagcgag ccctgactca ctacagtga gctgacaggg gotgtcatgc 450  
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
 acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550  
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600  
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650



atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700  
 gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750  
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800  
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950  
 gggatctgaa cagtttcggg gcttgoggaa gctgctgagt ttacatttac 1000  
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
 aacctggaac ttttggaact gggatataac cggatccgaa gtttagccag 1100  
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 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
 cagaaccttt acttgacgtg gaataaaatc agtgtcatag gacagaccat 1250  
 gtcctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300  
 tcgaagcttt cagtggaccc agtggtttcc agtgtgtccc gaatctgcag 1350  
 cgcctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400  
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 aatgcagcag aaatatgtgc tcccttgtaa actggctgaa aagttttaaa 1500  
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650  
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 ctcgatcatc tgctggttat ctacgtgtca tggaagcggg accctgagag 1850  
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 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000  
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 aaataccaca atcaatgtga agcttgaact cgggtttaat ataataccta 2300  
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 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

	200	205	210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu	Phe
	215	220	225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn	Lys
	230	235	240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser	Leu
	245	250	255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser	Gly
	260	265	270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn	Leu
	275	280	285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp	Ser
	290	295	300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp	Glu
	305	310	315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser	Phe
	320	325	330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys	Glu
	335	340	345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser	Ile
	350	355	360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala	Leu
	365	370	375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His	Glu
	380	385	390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro	Gly
	395	400	405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys	Ile
	410	415	420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile	Leu
	425	430	435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met	Lys
	440	445	450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys	Lys
	455	460	465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe	Tyr
	470	475	480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu	Leu
	485	490	495

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 386  
 ctgggatctg aacagtttcg gggc 24

<210> 387  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 387  
 ggtccccagg acatggtctg tccc 24

<210> 388  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 388  
 gctgagttaa catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
 <211> 1449  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtaacctca 100  
 gogatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
 ctoggacctc ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tcctgctgct ggtttttggtg 250  
 gcagctcttc tctgtggagc tgtgggtcctc tgcctccagt gctggctgag 300  
 gagaccccca attgattctc acaggcgcac catggcagtt tttgctgttg 350  
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400  
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttcctgctcc 450  
 atgttttggc cctttaggct cccacacctc atatgaagaa attgtaaaaa 500  
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650  
 ggatgttgga aaaaattttg gtcattggaga tgttttaata gtaaagtagc 700  
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaacca 750  
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
 tctgctttaa actctttcct agcatggggt ccataaaaaat tattataatt 900  
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
 tgtagataga aggtgaagga gattgctgaa gatataagagc acatataatg 1150  
 ccaacacggg gagaaaagaa aatttccctt tttacagtaa tgaatgtggc 1200  
 ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250  
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
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 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr  
 1 5 10 15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

cttttcagtgcacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial



aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150  
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agtatataac acgttttttg gacaagtga gaatgtttta tcattctgtc 1250  
atttgttctc aatagatgta actgtagac tacggctatt tgaaaaaatg 1300  
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350  
tataatggtg aaaataatgt tttgaaatca tgacccaaag aatgtattga 1400  
tttgactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450  
aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500  
attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550  
gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600  
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650  
aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700  
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tttgagaat ggaactcttg aggactttag ccagggtgtat ataataaagg 1800  
tacttttgtg ctgcattaaa ttgcttgga agtggttaaca ttatattata 1850  
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900  
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tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000  
accctaactt tgggtaattc tagtataaaa caaattatac ttttatttaa 2050  
atttcccttg tagcaaatct aattgccaca tggtgcccta tatttcatag 2100  
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actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200  
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser  
1 5 10 15



Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu  
20 25 30  
His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
35 40 45  
Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
50 55 60  
Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
65 70 75  
Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
80 85 90  
Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
95 100 105  
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
110 115 120  
Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
125 130 135  
Ser Gly Ser Ile Arg  
140

<210> 396  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 396  
cgcgccggg cgcgcggggt gagcgtgccg aggcggctgt ggcgcaggct 50  
tccagcccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100  
gggcccagac aaccgggcca tgcttccccg ggtgccaatg cgaggtggag 150  
accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
gggcccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
caccagcatc tcacccactg ccttctcccg ccttcgctac ctggagtcgc 400  
ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500  
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acctctcca caacctcatt cacgcctcg tgccccaccc cagaggggcc 600  
ggcctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700  
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gccagtggc ttccgtgagc taccgggcct gcaggctctg gacctgtcgg 850  
gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggctgagc 900  
tccctgcagg agctggacct ttccggcacc aacctgggtgc ccctgcctga 950  
ggcgtgctc ctccacctcc cggcactgca gagcgtcagc gtgggccagg 1000  
atgtgcggtg ccggcgctg gtgcgggagg gcacctaccc ccggaggcct 1050  
ggctccagcc ccaagggtgcc cctgcactgc gtagacaccc gggaatctgc 1100  
tgccaggggc ccaccatct tgtgacaaat ggtgtggccc agggccacat 1150  
aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200  
tgtgccaaaca ccagtgggga gcccgaggc ctatgtggca gcgtcaccac 1250  
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gcaaagtctc acccctttgt ctacgttgct tccccaaacc atgagcagag 1350  
ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccc 1400  
cttatcccc aagtgccttc cctcatgcct gggccggcct gaccgcgaat 1450  
gggcagaggg tgggtgggac cccctgctgc agggcagagt tcaggccac 1500  
tgggctgagt gtccccttg gcccatggcc cagtcactca ggggcgagtt 1550  
tcttttctaa catagccctt tctttgccat gagggcoatga ggcccgttc 1600  
atccttttct atttccctag aaccttaatg gtagaaggaa ttgcaaagaa 1650  
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cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900  
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ttcggagcct ctggaagctt agggcacatt ggttcagcc tagccagttt 2000  
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 ttgttgccct tttaacggag tgtcactttc aaccggcctc ccctaccctc 2350  
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 aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500  
 cccacaggg cagtgaagtc tgtcttcccc cacctgcta gcccatcatc 2550  
 tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95					100					105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110					115					120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125					130					135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140					145					150

Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser
				155					160					165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly
				170					175					180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg
				185					190					195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu
				200					205					210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe
				215					220					225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln
				230					235					240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly
				245					250					255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala
				260					265					270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp
				275					280					285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu
				290					295					300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg
				305					310					315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly
				320					325					330
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser
				335					340					345
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu							
				350										

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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 gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150  
 atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200  
 ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250  
 cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300  
 ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350  
 tttcaggcct aagatgaaag cctctagtct tgcccttcagc cttctctctg 400  
 ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450  
 ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500  
 ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550  
 gaatcttaag gaggactgag tctttgcaag acacaaagcc tgccaatcga 600  
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 aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700  
 ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgccac 750

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<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

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				20					25					30
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40					45
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55					60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70					75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85					90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403  
 <211> 28  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.  
  
 <400> 403  
 ctcctgtggt ctccagatTT caggccta 28  
  
 <210> 404  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
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aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcgccat ttacagacac gtagtgatt ctggaggctg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
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ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
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<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
1 5 10 15



Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala		20	25	30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr		35	40	45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp		50	55	60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala		65	70	75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly		80	85	90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg		95	100	105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser		110	115	120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met		125	130	135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu		140	145	150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly		155	160	165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile		170	175	180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro		185	190	195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr		200	205	210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu		215	220	225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu		230	235	240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg		245	250	255
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr		260	265	270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly		275	280	285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met		290	295	300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg				

Glu Met Ser Gly Val Ser Pro Phe  
320

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<210> 407
<211> 31
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-31  
<223> Synthetic construct.

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<400> 407
cgcggatccc gttatcgtct tgcgctactg c 31
```

```
<210> 408
<211> 34
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-34  
<223> Synthetic construct.

```
<400> 408
gcggaattct taaaatggac tgactccact catc 34
```

```
<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens
```

```
<400> 409
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tcctgcgcgc ggcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150
tagataatth tcgttgcca gaatgtgaat gtattgactg gagttagaga 200
agaaatgctg tggcatctgt tgtcgcaggt atattgttht ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtattht ccacattggc thttcttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgtthtagga agaacaggtg ctcgagthtg gctthtcatth ggthtcatgt 450
tgatgtthtg gtcacttatt gcttccatgt ggattcttht tgggtgcatat 500
gttaccctaaa atactgatgt ttatccggga ctagctgtgt thtttctaaaa 550
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Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 411  
 gtttgaggaa gctgggatac 20

<210> 412  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 412  
 ccaaactcga gcacctgttc 20

<210> 413  
 <211> 40  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-40  
 <223> Synthetic construct.

<400> 413  
 atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

10006172-100061

<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414

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100017213001

<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
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 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
                   20                  25                  30  
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
                   35                  40                  45  
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
                   50                  55                  60  
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
                   65                  70                  75  
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
                   80                  85                  90  
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
                   95                  100                  105  
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
                   110                  115                  120  
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
                   125                  130                  135  
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
                   140                  145                  150  
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
                   155                  160                  165  
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
                   170                  175                  180  
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
                   185                  190                  195  
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
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 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
                   215                  220

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

1000612.100001

<222> 1-21  
 <223> Synthetic construct.  
  
 <400> 416  
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 <210> 417  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
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 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 417  
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 <210> 418  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 418  
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 <210> 419  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 419  
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 <210> 420  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 420  
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<210> 421  
 <211> 46  
 <212> DNA  
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 <222> 1-46  
 <223> Synthetic construct.

<400> 421  
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<210> 422  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1528  
 <223> unknown base

<400> 422  
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<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

Met	Leu	Phe	Ser	Ala	Leu	Leu	Leu	Glu	Val	Ile	Trp	Ile	Leu	Ala
1				5				10					15	
Ala	Asp	Gly	Gly	Gln	His	Trp	Thr	Tyr	Glu	Gly	Pro	His	Gly	Gln
				20				25					30	
Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln
				35				40					45	
Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp
				50				55					60	
Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu
				65				70					75	
Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu

	80		85		90
Pro Ser Thr Leu Tyr	Leu Gly Gly Leu	Pro Arg Lys Tyr Val	Ala		
	95	100	105		
Ala Gln Leu His	Leu His Trp Gly Gln	Lys Gly Ser Pro Gly	Gly		
	110	115	120		
Ser Glu His Gln	Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu	His		
	125	130	135		
Ile Val His Tyr	Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu	Ala		
	140	145	150		
Ala Glu Arg Pro	Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile	Glu		
	155	160	165		
Val Gly Glu Thr	Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser	His		
	170	175	180		
Leu His Glu Val	Arg His Lys Asp Gln	Lys Thr Ser Val Pro	Pro		
	185	190	195		
Phe Asn Leu Arg	Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr	Phe		
	200	205	210		
Arg Tyr Asn Gly	Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser	Val		
	215	220	225		
Leu Trp Thr Val	Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu	Gln		
	230	235	240		
Leu Glu Lys Leu	Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu	Pro		
	245	250	255		
Ser Lys Leu Leu	Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu	Asn		
	260	265	270		
Gln Arg Met Val	Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser	Tyr		
	275	280	285		
Thr Thr Gly Glu	Met Leu Ser Leu Gly	Val Gly Ile Leu Val	Gly		
	290	295	300		
Cys Leu Cys Leu	Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys	Ile		
	305	310	315		
Arg Lys Lys Arg	Leu Glu Asn Arg Lys	Ser Val Val Phe Thr	Ser		
	320	325	330		
Ala Gln Ala Thr	Thr Glu Ala				
	335				

<210> 424  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 424  
 gtaaagtcgc tggccagc 18

<210> 425  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 425  
 cccgatctgc ctgctgta 18

<210> 426  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 426  
 ctgcactgta tggccattat tgtg 24

<210> 427  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 427  
 cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428  
 <211> 1073  
 <212> DNA  
 <213> Homo sapiens

<400> 428  
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctcogga tcagggaaca 200  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300  
 ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350  
 ggggtgaatg tacaacagca actgcaccca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatactg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccctt 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700  
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5				10						15
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
				35					40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
				50					55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
				65					70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200					205					

<210> 430  
 <211> 1257  
 <212> DNA  
 <213> Homo Sapien

<400> 430  
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 cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100  
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150  
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200  
 ctgcagctgc ccgcgccgtc gagcgccctct gagatcccca aggggaagca 250  
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350  
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgcgg agtgtacatt taaaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggtcac ttccgctaaa atgcagaaat gcatgctgtc 600  
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700  
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750  
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
ttattatgcc ttggaatggt tcaactaaat gacattttta ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
aagtggtttc aatatttttt ttagttggtt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
aatttgtaaa tgtaagaat tttttttata tctgttaaatt aaaaattatt 1250  
tccaaca 1257

<210> 431  
<211> 243  
<212> PRT  
<213> Homo Sapien

<400> 431  
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
1 5 10 15  
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
20 25 30  
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
35 40 45  
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
50 55 60  
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
65 70 75  
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
80 85 90  
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
95 100 105  
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
110 115 120  
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
				230					235					240
Leu	Pro	Lys												

<210> 432  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial Sequence

<400> 432  
 aggacttgcc ctcaggaa 18

<210> 433  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 433  
 cgcaggacag ttgtgaaaat a 21

<210> 434  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 434  
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 435  
 cccacctgta ccaccatgt 19  
  
 <210> 436  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 436  
 actccaggca ccatctgttc tccc 24  
  
 <210> 437  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 437  
 aagggtggc attcaagtc 19  
  
 <210> 438  
 <211> 19  
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 <400> 438  
 tgacctggca aaggaagaa 19  
  
 <210> 439  
 <211> 21  
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 <223> Synthetic oligonucleotide probe  
  
 <400> 439  
 cagccaccct ccagtccaag g 21  
  
 <210> 440  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence



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<220>
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<400> 440
    gggtcgtggtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 441
    ctggccctca gagcaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
    tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
    ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
    aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

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<400> 445  
 agcgtacact ctctccaggc aaccag 26

<210> 446  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 446  
 caattctgga tgaggtggta ga 22

<210> 447  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 447  
 caggactgag cgcttggtta 20

<210> 448  
 <211> 21  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 448  
 caaagcgcca agtaccggac c 21

<210> 449  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 449  
 ccagacctca gccaggaa 18

<210> 450  
 <211> 18  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 450  
 ccctagctga ccccttca 18

<210> 451  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 451  
 tctgacaagc agttttctga atc 23

<210> 452  
 <211> 26  
 <212> DNA  
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<220>  
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<400> 452  
 ctctccccct cccttttcct ttgttt 26

<210> 453  
 <211> 18  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 453  
 ctctggtgcc cacagtga 18

<210> 454  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 454  
 ccatgcctgc tcagccaaga a 21

<210> 455  
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 <212> DNA  
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<220>  
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<400> 455  
 caggaaatct ggaaacctac agt 23

<210> 456  
 <211> 20  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456  
ccttgaaaag gaccagttt 20

<210> 457  
<211> 22  
<212> DNA  
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<220>

<223> Synthetic oligonucleotide probe

<400> 457  
atgagtcgca cctgctgttc cc 22

<210> 458  
<211> 18  
<212> DNA  
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<220>

<223> Synthetic oligonucleotide probe

<400> 458  
tagcagctgc ccttggtta 18

<210> 459  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459  
aacagcaggt gcgactcatc ta 22

<210> 460  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460  
tgctaggcga cgacacccag acc 23

<210> 461  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>



aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

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<210> 468

<211> 19

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<223> Synthetic oligonucleotide probe

<400> 468

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<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 472  
 tcagggtcta catcagcctc ctgc 24  
  
 <210> 473  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 473  
 aaggccaagg tgagtccat 19  
  
 <210> 474  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 474  
 cctactgagg agccctatgc 20  
  
 <210> 475  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 475  
 tccaggtgga cccacttca gg 22  
  
 <210> 476  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 476  
 gggaggctta taggcccaat ctgg 24  
  
 <210> 477  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

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